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(54) Title: GENES INVOLVED IN TOLERANCE TO ENVIRONMENTAL STRESS		
(57) Abstract <p>The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table 1 as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.</p>		

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Genes involved in tolerance to environmental stress

The present invention relates to molecular biology, in particular plant
5 molecular biology. In particular, the invention relates to improvements of crop
productivity of useful plants. One of the major limitations of crop productivity is the
effect of environmental stress conditions on plant growth and development. An
important goal of molecular biology is the identification and isolation of genes that can
provide resistance or tolerance to such stresses. For agriculture, the creation of
10 transgenic plants containing such genes provides the potential for improving the stress
resistance or tolerance of plants.

Drought, salt loading, and freezing are stresses that cause adverse effects on
the growth of plants and the productivity of crops. The physiological response to these
stresses arises out of changes in cellular gene expression. Expression of a number of
15 genes has been demonstrated to be induced by these stresses (Zhu et al., 1997;
Shinozaki et al., 1996; Thomashow, 1994). The products of these genes can be
classified into two groups: those that directly protect against environmental stresses
and those that regulate gene expression and signal transduction in the stress
response. The first group includes proteins that likely function by protecting cells from
20 dehydration, such as the enzymes required for biosynthesis of various
osmoprotectants, late-embryogenesis-abundant (LEA) proteins, antifreeze proteins,
chaperones, and detoxification enzymes (Shinozaki et al., 1997, Ingram et al., 1996,
Bray et al., 1997). The second group of gene products includes transcription factors,
protein kinases, and enzymes involved in phosphoinositide metabolism (Shinozaki et
25 al., 1997). An overview of the methods known to improve stress tolerance in plants is
also given in Holmberg & Bülow, (1998).

Further studies are definitely needed to give an insight into the mechanisms
involved in the plant response to environmental stress conditions.

The study of plants naturally adapted to extreme desiccation has led to the
30 hypothesis that the genetic information for tolerance to environmental stress conditions
exists in all higher plants. In glycophytes, this information would only be expressed in
seeds and pollen grains which undergo a desiccation process.

The induction of osmotolerance in plants is very important to crop productivity:
30 to 50 % of the land under irrigation is presently affected by salinity. Several lines of
35 evidence also demonstrate that even mild environmental stress conditions throughout
the growth season have a negative impact on plant growth and crop productivity. It is

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for instance known that even minor limitations in water availability cause a reduced photosynthetic rate. Unpredictable rainfall, increase in soil salinity at the beginning and the end of the growing season often result in decreased plant growth and crop productivity. These environmental factors share at least one element of stress and that is water deficit or dehydration. Drought is a significant problem in agriculture today. Over the last 40 years, for example, drought accounted for 74% of the total US crop losses of corn. To sustain productivity under adverse environmental conditions, it is important to provide crops with a genetic basis for coping with water deficit, for example by breeding water retention and tolerance mechanisms into crops so that they can grow and yield under these adverse conditions.

It is an aim of the present invention to provide a new method for screening for plant genes involved in tolerance or resistance to environmental stress.

It is an aim of the present invention to provide new plant genes, more particularly plant genes providing the potential of improving the tolerance to environmental stress conditions in plants.

It is also an aim of the present invention to provide polypeptides encoded by said new plant genes.

It is further an aim of the present invention to provide methods for producing plants with enhanced tolerance or resistance to environmental stress conditions based on said new genes.

It is also an aim of the present invention to provide recombinant polynucleic acids comprising said new genes.

It is further an aim of the present invention to provide plant cells and plants transformed with said new genes.

It is further an aim of the present invention to provide plant cells and plants with enhanced tolerance or resistance to environmental stress conditions.

The present invention relates more particularly to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

It has been found that the transfer of genes from plants which are often difficult to assay for certain characteristics, to lower eukaryotes, such as yeasts and fungi, but

in particular yeast, especially *Saccharomyces*, is relatively easy to achieve, whereby it has now been shown that the results of testing for tolerance or resistance to environmental conditions in the resulting yeast cells gives a relatively reliable measure of the capability of the inserted coding sequence or gene to induce tolerance or resistance to environmental stress in plants. Thus the expression of polynucleic acid sequences comprising the gene or coding sequence which are responsible for inducing tolerance or resistance to environmental stress conditions can be enhanced in the plant species from which it originates or in any other plant species.

In the present context the term "enhancing" must be understood to mean that the levels of molecules correlated with stress protection in a transformed plant cell, plant tissue or plant part will be "substantially increased" or "elevated" meaning that this level will be greater than the levels in an untransformed plant.

This may be achieved by inducing overexpression of suitable genetic information which is already present, or by any other suitable means of introducing into the plant cell heterologous information resulting in a capability to tolerate or resist environmental stress.

The term "environmental stress" has been defined in different ways in the prior art and largely overlaps with the term "osmotic stress". Holmberg et al., 1998 for instance define different environmental stress factors which result in abiotic stress. Salinity, drought, heat, chilling and freezing are all described as examples of conditions which induce osmotic stress. The term "environmental stress" as used in the present invention refers to any adverse effect on metabolism, growth or viability of the cell, tissue, seed, organ or whole plant which is produced by a non-living or non-biological environmental stressor. More particularly, it also encompasses environmental factors such as water stress (flooding, drought, dehydration), anaerobic (low level of oxygen, CO₂ etc.), aerobic stress, osmotic stress, salt stress, temperature stress (hot/heat, cold, freezing, frost) or nutrients/pollutants stress.

The term "anaerobic stress" means any reduction in oxygen levels sufficient to produce a stress as hereinbefore defined, including hypoxia and anoxia.

The term "flooding stress" refers to any stress which is associated with or induced by prolonged or transient immersion of a plant, plant part, tissue or isolated cell in a liquid medium such as occurs during monsoon, wet season, flash flooding or excessive irrigation of plants, etc.

"Cold stress" and "heat stress" are stresses induced by temperatures which are respectively, below or above, the optimum range of growth temperatures for a

particular plant species. Such optimum growth temperature ranges are readily determined or known to those skilled in the art.

“Dehydration stress” is any stress which is associated with or induced by the loss of water, reduced turgor or reduced water content of a cell, tissue, organ or whole
5 plant.

“Drought stress” refers to any stress which is induced by or associated with the deprivation of water or reduced supply of water to a cell, tissue, organ or organism.

“Oxidative stress” refers to any stress which increases the intracellular level of reactive oxygen species.

10 The terms “salinity-induced stress”, “salt-stress” or similar term refer to any stress which is associated with or induced by elevated concentrations of salt and which result in a perturbation in the osmotic potential of the intracellular or extracellular environment of a cell.

Said salt can be for example, water soluble inorganic salts such as sodium
15 sulfate, magnesium sulfate, calcium sulfate, sodium chloride, magnesium chloride, calcium chloride, potassium chloride etc., salts of agricultural fertilizers and salts associated with alkaline or acid soil conditions.

The transgenic plants obtained in accordance with the method of the present invention, upon the presence of the polynucleic acid and/or regulatory sequence
20 introduced into said plant, attain resistance, tolerance or improved tolerance or resistance against environmental stress which the corresponding wild-type plant was susceptible to.

The terms “tolerance” and “resistance” cover the range of protection from a delay to complete inhibition of alteration in cellular metabolism, reduced cell growth
25 and/or cell death caused by the environmental stress conditions defined herein before. Preferably, the transgenic plant obtained in accordance with the method of the present invention is tolerant or resistant to environmental stress conditions in the sense that said plant is capable of growing substantially normal under environmental conditions where the corresponding wild-type plant shows reduced growth, metabolism, viability,
30 productivity and/or male or female sterility. Methodologies to determine plant growth or response to stress include, but are not limited to height measurements, leaf area, plant water relations, ability to flower, ability to generate progeny and yield or any other methodology known to those skilled in the art.

The terms “tolerance” and “resistance” may be used interchangeably in the
35 present invention.

The methods according to the invention as set out below can be applied to any, higher plant, preferably important crops, preferably to all cells of a plant leading to an enhanced osmotic or any other form of environmental stress tolerance. By means of the embodiments as set out below, it now becomes possible to grow crops with improved yield, growth, development and productivity under environmental stress conditions, it may even become possible for instance to grow crops in areas where they cannot grow without the induced osmotolerance according to the invention.

In order to do a thorough screening for relevant plant genes and/or coding sequences, it is preferred to apply a method according to the invention whereby said cDNA library comprises copies of essentially all mRNA of said plant cell. Probably only coding sequences are sufficient. For the screening of genes involved in environmental stress, it is preferred to use a cDNA library from siliques (fruits, containing the maturing seeds), such as the siliques from *Arabidopsis*, because genes involved in for instance osmotolerance are preferentially expressed in these organs.

Although the genetic information may be introduced into yeast for screening by any suitable method, as long as it is in a functional format long enough for testing of tolerance or resistance to environmental stress conditions, it is preferred for ease of operation to use a well known vector such as a 2 μ plasmid. It is to be preferred to have the coding sequence or the gene under control of a strong constitutive yeast promoter, to enhance good expression of the gene or coding sequence of interest. Strong constitutive yeast promoters are well known in the art and include, but are not limited to the yeast TPI promoter.

The term "gene" as used herein refers to any DNA sequence comprising several operably linked DNA fragments such as a promoter and a 5' untranslated region (the 5'UTR), a coding region (which may or may not code for a protein), and an untranslated 3' region (3'UTR) comprising a polyadenylation site. Typically in plant cells, the 5'UTR, the coding region and the 3'UTR (together referred to as the transcribed DNA region) are transcribed into an RNA which, in the case of a protein encoding gene, is translated into a protein. A gene may include additional DNA fragments such as, for example, introns. As used herein, a genetic locus is the position of a given gene in the genome of a plant.

The present invention more particularly relates to an isolated polynucleic acid obtainable by a method comprising the preparation of a cDNA as set out above comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an

enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

The term "polynucleic acid" refers to DNA or RNA, or amplified versions thereof, or the complement thereof.

5 The present invention more particularly provides an isolated polynucleic acid obtainable by a method as defined above which encodes a polypeptide as listed in Table 1.

10 The capacity of an isolated polynucleic acid to confer tolerance or resistance to environmental stress conditions can be tested according to methods well-known in the art, see for example, Grillo et al. (1996), Peassarakli et al. (Editor), Nilsen et al. (1996), Shinozaki et al. (1999), Jones et al. (1989), Fowden et al. (1993) or as described in the appended examples.

15 The present invention more particularly relates to an isolated polynucleic acid which encodes a homolog of any of the polypeptides as listed in Table 1, which is chosen from:

- (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, or 121, or the complementary strands thereof;
- 20 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- 25 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

30 Said fragment as defined above are preferably unique fragments of said sequences.

The term "hybridizing" refers to hybridization conditions as described in Sambrook (1989), preferably specific or stringent hybridization conditions are aimed at.

Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which
5 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least about 60°C.

In the present invention, genomic DNA or cDNA comprising the polynucleic acids of the invention can be identified in standard Southern blots under stringent
10 conditions using the cDNA sequence shown. The preparation of both genomic and cDNA libraries is within the skill of the art. Examples of hybridization conditions are also given in the Examples section.

The present invention also relates to the isolated polynucleic acids which encode polypeptides which are a homolog of the polypeptides as set out in Table 1
15 useful for the production of plants which are resistant or tolerant to environmental stress conditions.

The present invention also relates to a polynucleic acid comprising at least part of any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or
20 at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121. Preferably, said gene encodes a protein having
25 substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76 or 78. Said part of said gene is preferably a unique part.

The present invention preferably relates to the use of a polynucleic acid
30 comprising at least part of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%,
35 80% or 85% identical, and most preferably at least 90% or 95% identical to any of

SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121 for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

The present invention particularly relates to an isolated polynucleic acid as defined above, which encodes a plant homolog of yeast DBF2 kinase, more particularly a DBF2 kinase homolog from *Arabidopsis thaliana* termed At-DBF2, which can at least be used to confer enhanced environmental stress tolerance or resistance in plants and yeast.

More preferably, the present invention relates to an isolated polynucleic acid encoding a plant DBF2 kinase, which is chosen from:

- (a) SEQ ID NO 1, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- (c) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

Alternatively, the present invention relates to a polynucleic acid derived from a plant comprising at least part of SEQ ID NO 1, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 1. Preferably said gene encodes a protein

having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2.

The present invention also relates to the use of an isolated polynucleic acid as defined above which encodes a plant HSP 17.6A protein for the production of transgenic plants, more particularly a homolog from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 10 (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 15 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to the use of a polynucleic acid comprising at least part of SEQ ID NO 3, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 3. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 4, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 35 (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;

- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

5 for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

10 The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more
15 preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

20 Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

25 According to another preferred embodiment, the present invention relates to an isolated polynucleic acid as defined above, which encodes a protein termed c74, more particularly a plant homolog of c74, even more preferably a c74 from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More particularly, the present invention relates to an isolated polynucleic acid as defined above, which is chosen from:

30

- (a) SEQ ID NO 5, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to a polynucleic acid comprising at least part of SEQ ID NO 5, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 5. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 6.

Two nucleic acid sequences or polypeptides are said to be "identical" according to the present invention if the sequence of nucleotides or amino acid residues, respectively, in the two sequences is the same when aligned for maximum correspondence as described below. The term "complementary to" is used herein to mean that the complementary sequence hybridizes to all or a portion of a given polynucleotide sequence.

Sequence comparisons between two (or more) polynucleic acid or polypeptide sequences are typically performed by comparing sequences of the two sequences over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981), by the homology alignment algorithm of Needleman and Wunsch (1970), by the search for similarity method of Pearson and Lipman (1988), by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by visual inspection.

"Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleic acid or polypeptide sequences in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not
5 comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the
10 percentage of sequence identity.

The term "substantial identity" of polynucleic acid or polypeptide sequences means that a polynucleotide sequence comprises a sequence that has at least 60%, 65%, 70% or 75% sequence identity, preferably at least 80% or 85%, more preferably at least 90% and most preferably at least 95 %, compared to a reference sequence
15 using the programs described above (preferably BLAST) using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means
20 sequence identity of at least 40%, 45%, 50% or 55% preferably at least 60%, 65%, 70%, 75%, 80% or 85% more preferably at least 90%, and most preferably at least 95%. Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of
25 residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and
30 tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other, or a third nucleic acid, under stringent conditions.

More particularly, the polynucleic acids as used herein will comprise at least part of a DNA sequence which is essentially similar, or, preferentially, essentially
5 identical or identical to one or both of the nucleotide or amino acid sequences corresponding to SEQ ID NO 1 to 121 disclosed herein, more specifically in the nucleotide sequence encoding, or the amino-acid sequence corresponding to the "active domain" of the respective protein or polypeptide.

The polynucleic acid sequences according to the present invention can be
10 produced by means of any nucleic acid amplification technique known in the art such as PCR or conventional chemical synthesis.

For a general overview of PCR see PCR Protocols (Innis et al. (1990)).

Polynucleotides may also be synthesized by well-known techniques as described in the technical literature. See, e.g., Carruthers et al. (1982) and Adams et
15 al. (1983). Double stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

The present invention more particularly relates to an isolated polypeptide
20 encoded by a polynucleic acid according to any of the polynucleic acids as defined above, or a functional fragment thereof.

The present invention preferably relates to an isolated polypeptide as listed in Table 1 or to an isolated polypeptide encoded by a polynucleic acid isolated as defined above. Preferably, the present invention relates to polypeptides or peptides having at
25 least part of the sequence of any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Preferably, said part is a unique part and preferably includes the active domain of said polypeptide. Preferably said polypeptide is a
30 recombinant polypeptide.

The term "isolated" distinguishes the protein or polynucleic acid according to the invention from the naturally occurring one.

The present invention also relates to a polypeptide comprising at least part of a polypeptide which is at least 50%, 55%, 60%, 65% identical, preferentially at least
35 70%, 75% identical, more preferably at least 80% or 85% identical, and most

preferably at least 90% or 95% identical to any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

5 The terms "polypeptide" and "protein" are used interchangeably throughout the present description.

Said polypeptide preferably has the ability to confer tolerance or resistance to environmental stress conditions in at least plants, plant parts, plant tissues, plant cells, plant calli or yeast.

10 The term "functional fragment" refers to a fragment having substantially the biological activity of the protein from which it is derived.

The polypeptides of the present invention may be produced by recombinant expression in prokaryotic and eukaryotic engineered cells such as bacteria, yeast or fungi. It is expected that those of skill in the art are knowledgeable in the numerous
15 expression systems available for expression in these systems.

The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell
20 enhances tolerance or resistance to environmental stress of said plant.

The term "plant cell" as defined above also comprises plant tissue or a plant as a whole. The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any
25 of the polynucleic acids encoding a protein as listed in Table 1 which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress in said plant.

The term "(over)expression" refers to the fact that the polypeptides of the invention encoded by said polynucleic acid are preferably expressed in an amount
30 effective to confer tolerance or resistance to the transformed plant, to an amount of salt, heat, cold, (or other stress factors) that inhibits the growth of the corresponding untransformed plant.

Several methods to obtain transient introduction and expression of a recombinant DNA in a plant are known to the art. For example, plant virus vectors can

be used to obtain such purpose. Examples conferring to the use of plant viral vectors are described in Porta and Lomonosoff (1996), WO9320217 and US 5,589,367.

The present invention also relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising stably
5 introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances the environmental stress tolerance or resistance of a plant.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method
10 comprising introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed Table 1 which when (over)expressed in a plant cell enhances the environmental stress resistance of said plant.

According to a preferred embodiment, the present invention relates to a
15 method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a DBF2 kinase, preferably a plant DBF2 kinase, most preferably an Arabidopsis DBF2 kinase.

According to another preferred embodiment, the present invention relates to a
20 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding an HSP 17.6A protein, preferably a plant HSP 17.6A protein, most preferably an Arabidopsis HSP 17.6A.

According to a preferred embodiment, the present invention relates to a
25 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a c74 protein, preferably a plant c74 protein, most preferably a Arabidopsis c74 protein.

Preferably, the present invention relates to a method as defined above,
30 comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a polynucleic acid as defined above, and,
- a plant expressible promoter, whereby said
35 polynucleic acid is in the same transcriptional unit

and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

The present invention also relates to a method for producing a plant with enhanced
5 tolerance or resistance to environmental stress, said method comprising indirectly
increasing or inducing the expression of an endogenous gene in said plant comprised
within a polynucleic acid as defined above or indirectly increasing or inducing the activity
of a protein as defined above.

The present invention also relates to a method as defined above, comprising:

10 (a) introducing into the genome of a plant cell one or more recombinant DNA
molecules, said recombinant DNA molecules comprising:

- 15 - a DNA encoding a protein which when expressed in
said plant cell at an effective amount indirectly
increases or induces the expression of an
endogenous polynucleic acid or indirectly increases
or induces the protein activity of a protein encoded by
said polynucleic acid of the present invention, and,
- 20 - a plant expressible promoter, whereby said DNA is in
the same transcriptional unit and under the control of
said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

A "recombinant" DNA molecule will comprise a "heterologous sequence"
meaning that said recombinant DNA molecule will comprise a sequence originating
from a foreign species, or, if from the same species, may be substantially modified
25 from its original form. For example, a promoter operably linked to a structural gene
which is from a species different from which the structural gene was derived, or, if
from the same species, may be substantially modified from its original form.

The present invention also relates to a method as defined above for producing
a plant with enhanced tolerance or resistance to environmental stress conditions, said
30 method comprising indirectly increasing or inducing the expression of an endogenous
gene in said plant comprised within a polynucleic acid as defined above or indirectly
increasing or inducing the activity of a protein of the invention as defined above.
According to this embodiment, other polynucleic acids modulating the expression or
the activity of a protein according to the present invention may be introduced

transiently or stably into the genome of said plants. The term "modulating" means enhancing, inducing, increasing, decreasing or inhibiting.

Increase or induction of expression or induction or increase of protein activity is required when said regulator protein is a positive regulator of the expression or the activity of at least one of the polynucleic acids or protein of the present invention.

Decrease or inhibition of expression or decrease or inhibition of protein activity is required when said regulator protein is a negative regulator of the expression or activity of at least one of the polynucleic acids or proteins of the present invention.

Increase of the activity of said polypeptide according to the present invention is obtained, according to one embodiment of the invention, by influencing endogenous gene expression in the plant. This is preferably achieved by the introduction of one or more polynucleic acid sequences according to the invention into the plant genome, in a suitable conformation for gene expression (e.g. under control of a plant-expressible promoter). This will result in increased or induced expression (overexpression) or increased or induced activity of the protein in the plant cells, and, in the presence of an adequate substrate, in an increase of tolerance or resistance to environmental stress conditions in a transgenic plant or plant cell as compared to a non-transgenic plant or plant cell. This increase in tolerance can be measured by measuring mRNA levels, or where appropriate, the level or activity of the respective protein (e.g. by means of ELISA, activity of the enzyme as measured by any technique known in the art). Endogenous gene expression refers to the expression of a protein which is naturally found in the plant, plant part or plant cell concerned.

Alternatively, said enhanced tolerance or resistance to environmental stress conditions may be achieved by introducing into the genome of the plant, one or more transgenes which interact with the expression of endogenous genes (polynucleic acids) according to the present invention, by anti-sense RNA, co-suppression or ribozyme suppression of genes which normally inhibit the expression of the polynucleic acids of the present invention or by suppression of genes which normally inhibit the activity of the polypeptides of the invention as defined above.

For inhibition of expression, the nucleic acid segment to be introduced generally will be substantially identical to at least a portion of the endogenous gene or genes to be repressed. The sequence, however, need not be perfectly identical to inhibit expression. The vectors of the present invention can be designed such that the inhibitory effect applies to other genes within a family of genes exhibiting homology or substantial homology to the target gene.

For antisense suppression, the introduced sequence also need not be full length relative to either the primary transcription product or fully processed mRNA.

Generally, higher homology can be used to compensate for the use of a shorter sequence.

5 Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments may be equally effective. Normally, a sequence of between about 30 or 40 nucleotides up to the full length sequence should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of
10 about 500 to about 1700 nucleotides is especially preferred.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of genes as explained above. It is possible to design ribozymes that specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage,
15 the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs.

A number of classes of ribozymes have been identified. One class of
20 ribozymes is derived from a number of small circular RNAs which are capable of selfcleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and
25 subterranean clover mottle virus. The design and use of target RNA-specific ribozymes is described in Haseloff et al. (1988).

Another method of suppression of gene expression is sense suppression. Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to block the transcription of target genes. For an example
30 of the use of this method to modulate expression of endogenous genes see, Napoli et al. (1990), and U.S. Patents Nos. 5,034,323, 5,231,020, and 5,283,184.

The suppressive effect may occur where the introduced sequence contains no coding sequence per se, but only intron or untranslated sequences homologous to sequences present in the primary transcript of the endogenous sequence. The
35 introduced sequence generally will be substantially identical to the endogenous

sequence intended to be repressed. This minimal identity will typically be greater than about 65%, but a higher identity might exert a more effective repression of expression of the endogenous sequences. Substantially greater identity of more than about 80% is preferred, though about 95% to absolute identity would be most preferred. As with
5 antisense regulation, the effect should apply to any other proteins within a similar family of genes exhibiting homology or substantial homology.

For sense suppression, the introduced sequence, needing less than absolute identity, also need not be full length, relative to either the primary transcription product or fully processed mRNA. This may be preferred to avoid concurrent production of
10 some plants which are overexpressers. A higher identity in a shorter than full length sequence compensates for a longer, less identical sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and identity of non-coding segments will be equally effective. Normally, a sequence of the size ranges noted above for antisense regulation is used.

15 Other methods for altering or replacing genes known in the art can also be used to inhibit expression of a gene. For instance, insertional mutants using T-DNA or transposons can be generated. See, e.g., Haring et al. (1991) and Walbot (1992). Another strategy in genetic engineering of plants and animals is targeted gene replacement. Homologous recombination has typically been used for this purpose
20 (see, Capecchi (1989)).

Alternatively, the present invention also relates to a method as defined above wherein said DNA encodes a sense or antisense RNA or a ribozyme capable of indirectly increasing or inducing the expression of an endogenous polynucleic acid sequence according to the invention as defined above or increasing or inducing the
25 activity of a protein of the invention as defined above. Preferably said endogenous polynucleic acid encodes a protein as listed in Table 1.

The present invention also relates to a recombinant polynucleic acid comprising: a polynucleic acid as defined above, and, a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control
30 of said plant-expressible promoter.

The present invention also relates to a recombinant polynucleic acid comprising:

(a) a DNA encoding a protein which when expressed in said plant at an effective amount indirectly increases or induces the expression of an endogenous

polynucleic acid as defined above or indirectly increases or induces the protein activity of a polypeptide as defined above, and,

(b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

5 An "endogenous" polynucleic acid refers to a polynucleic acid that is already present in the plant species before transformation.

Said recombinant polynucleic acid as described here above is generally also referred to as a "recombinant vector" or an "expression cassette". An expression cassette of the invention can be cloned into an expression vector by standard
10 methods. The expression vector can then be introduced into host cells by currently available DNA transfer methods.

The present invention also relates to the recombinant polynucleic acid as defined above, comprising a DNA which encodes an anti-sense RNA, a ribozyme or a sense RNA which increases or induces the activity of a protein as defined above in
15 said cell. Preferably said protein is listed in Table 1.

More particularly, the present invention relates to a recombinant polynucleic acid comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99,
20 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121.

Preferably, the present invention relates to a recombinant polynucleic acid comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1. Preferably, said "part" is a unique part of any of said nucleotide sequences. (26-28) As used herein, the term a "plant-expressible promoter" refers to a promoter
25 that is capable of driving transcription in a plant cell. This includes any promoter of plant origin, including the natural promoter of the transcribed DNA sequence, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell. The promoter may also be an artificial or synthetic promoter. The term "plant-expressible promoter" includes, but is not restricted to, constitutive, inducible, organ-,
30 tissue-specific or developmentally regulated promoters.

According to the invention, production and/or activity of a polypeptide according to the present invention in a plant or in plant parts is increased by introducing *one or more* polynucleic acids according to the invention into the genome of the plant. More specifically, the constitutive promoter can be, but is not restricted to, one of the
35 following: a 35S promoter (Odell et al. (1985)), a 35S'3 promoter (Hull and Howell

(1987)), the promoter of the nopaline synthase gene ("PNOS") of the Ti-plasmid (Herrera -Estrella, (1983)) or the promoter of the octopine synthase gene ("POCS", De Greve et al. (1982)). It is clear that other constitutive promoters can be used to obtain similar effects. A list of plant-expressible promoters that can be used according to the present invention is given in Table 2.

For specific embodiments of this invention, the use of inducible promoters can provide certain advantages. Modulation of protein levels or protein activity may be required in certain parts of the plant, making it possible to limit modulation to a certain period of culture or developmental stage of the plant.

For specific embodiments of this invention, the use of organ- or tissue-specific or chemical inducible promoters can provide certain advantages. Thus, in specific embodiments of the invention, the gene(s) or part thereof is (are) placed under the control of a promoter directing expression in specific plant tissues or organs, such as for instance roots, leaves, harvestable parts, etc.

It is also possible to use a promoter that can be induced upon the environmental stress conditions. Such promoters can be taken for example from stress-related genes which are regulated directly by an environmental, i.e. preferable abiotic, stress in a plant cell, including genes for which expression is increased, reduced or otherwise altered. These stress related genes comprise genes the expression of which is either induced or repressed by anaerobic stress, flooding stress, cold stress, dehydration stress, drought stress, heat stress or salinity. An exemplary list of such promoters is given in Table 3.

The recombinant polynucleic acids according to the present invention may include further regulatory or other sequences from other genes, such as leader sequences (e.g. the cab22 leader from Petunia), 3' transcription termination and polyadenylation signals (e.g. from the octopine synthase gene or the nopaline synthase gene), plant translation initiation consensus sequences, introns, transcription enhancers and other regulatory elements such as adh intron 1, etc, which is or are operably linked to the gene or a fragment thereof. Additionally, the recombinant polynucleic acid can be constructed and employed to target the gene product of the polynucleic acid of the invention to a specific intracellular compartment within a plant cell or to direct a protein to the extracellular environment. This can generally be obtained by operably joining a DNA sequence encoding a transit or signal peptide to the recombinant polynucleic acid.

The recombinant DNA comprising one or more polynucleic acids according to the present invention may be accompanied by a chimeric marker gene (Hansen et al., 1999 and references therein). The chimeric marker gene can comprise a marker DNA that is operably linked at its 5' end to a plant-expressible promoter, preferably a
5 constitutive promoter, such as the CaMV 35S promoter, or a light inducible promoter such as the promoter of the gene encoding the small subunit of Rubisco; and operably linked at its 3' end to suitable plant transcription 3' end formation and polyadenylation signals. It is expected that the choice of the marker DNA is not critical, and any suitable marker DNA can be used. For example, a marker DNA can encode a protein
10 that provides a distinguishable color to the transformed plant cell, such as the A1 gene (Meyer et al., (1987)), can provide herbicide resistance to the transformed plant cell, such as the *bar* gene, encoding resistance to phosphinothricin (EP 0 242 246), or can provide antibiotic resistance to the transformed cells, such as the *aac(6')* gene, encoding resistance to gentamycin (WO94/01560).

15 According to another embodiment, the present invention relates to the use of the polynucleic acids above as selectable marker gene. More preferably, the present invention also relates to the use of the plant DBF2 gene as defined above as selectable marker gene, selection taking place with treatment with a stress condition.

20 The recombinant DNA vectors according to the present invention comprising the sequences from genes of the invention will typically also comprise a marker gene which confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance
25 to chlorosulfuron or Basta.

The present invention also relates to a recombinant host cell transformed with an isolated polynucleic acid as defined above. Said host can be any host known in the art. Preferably said recombinant host cell is a plant cell, yeast, fungi, insect cell, etc. In order to be efficiently expressed in said host, said polynucleic acids can be combined
30 with any promoter known to function in said host system. Methods for transforming said host cells are also well known in the art.

The present invention particularly also relates to a plant cell transformed with at least one recombinant polynucleic acid as defined above.

35 The present invention also relates to a plant consisting essentially of plant cells transformed with at least one recombinant polynucleic acid as defined above.

A "transgenic plant" refers to a plant comprising a transgene in the genome of essentially all of its cells.

DNA constructs of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques (see for example Hansen et al., 1999 for review and WO 99/05902). For example, DNA constructs of the invention may be introduced into the genome of the desired plant host by using techniques such as protoplast transformation, biolistics or microprojectile bombardment or Agrobacterium mediated transformation.

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. (1984).

Electroporation techniques are described in Fromm et al. (1985). Biolistic transformation techniques are described in Klein et al. (1987).

Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional Agrobacterium host vector. The virulence functions of the Agrobacterium host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. Agrobacterium tumefaciens-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Horsch et al. (1984), and Fraley et al. (1983).

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium. Plant regeneration from cultured protoplasts is described in Evans et al. (1983); and Binding (1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. (1987).

The polynucleic acids and polypeptides of the invention can be used to confer desired traits on a broad range of plants, including monocotyledonous or dicotyledonous plants, preferably they belong to a plant species of interest in agriculture, wood culture or horticulture, such as a crop plant, root plant, oil producing plant, wood producing plant, fruit producing plant, fodder or forage legume, companion or ornamental or horticultured plant. The plants can include species from the genera Actinidia, Apium, Allium, Ananas, Arachis, Arisaema, Asparagus, Atropa, Avena, Beta,

Brassica, Carica, Cichorium, Citrus, Citrullus, Capsicum, Cucumis, Cucurbita, Cydonia, Daucus, Diospyros, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyamus, Ipomoea, Lactuca, Linum, Lolium, Lycopersicon, Malus, Mangifera, Manihot, Majorana, Medicago, Musa, Nicotiana, Oryza, Panicum, Pannesetum, Persea, Petroselinum, Phaseolus, Pisum, Pyrus, Prunus, Raphanus, Rheum, Ribes, Rubus, Saccharum, Secale, Senecio, Sinapis, Solanum, Sorghum, Spinacia, Trigonella, Triticum, Vaccinium, Vitis, Vigna, Zea, and Zingiber. Additional species are not excluded. Crops grown on cultivated lands in arid and semi-arid areas in which irrigation with ground water is needed may advantageously benefit from the invention.

One of skill will recognize that after the recombinant polynucleic acid is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. As described before, the plant cells, plant tissue, in particular, transgenic plants of the invention display a certain higher or enhanced degree of tolerance (or even resistance) to environmental stress conditions compared to the corresponding wild-type plants. For the meaning of "environmental stress", see supra. In a preferred embodiment of the present invention, the transgenic plant displays increased tolerance to osmotic stress, salt stress, cold and/or heat stress. An increase in tolerance to such environmental stress is understood to refer to a tolerance to a level of such stress which inhibits the growth and productivity of the corresponding untransformed plant, as determined by methodologies known to the art. Such increased tolerance in transgenic plants is related to an increased expression level in the transgenic plant or parts thereof of one or more of the polynucleic acids of the present invention and/or to an increased level of activity of the polypeptide(s) encoded by said polynucleic acid, as determined by methodologies known to the art. In comparison with their untransformed counterparts, and determined according to methodologies known in the art, a transgenic plant according to the present invention shows an increased growth, viability, metabolism, fertility and/or productivity under mild environmental stress conditions. In the alternative, a transgenic plant according to the invention can grow under environmental stress conditions wherein the untransformed counterparts can not grow. An increase in tolerance to salt stress is understood to refer to the capability of the transgenic plant to grow under stress conditions which inhibit the growth of at least 95% of the parent, non-stress tolerant plants from which the stress tolerant transgenic

plants are derived. Typically, the growth rate of stress tolerant plants of the invention will be inhibited by less than 50%, preferably less than 30%, and most preferably will have a growth rate which is not significantly inhibited by growth conditions which inhibit the growth of at least 95% of the parental, non-stress tolerant plants. In an alternative
5 example, under mild environmental stress conditions, the growth and/or productivity of the transgenic plants is statistically at least 1 % higher than for their untransformed counterparts, preferably more than 5 % higher and most preferably more than 10 % higher.

Any transformed plant obtained according to the invention can be used in a
10 conventional breeding scheme or in *in vitro* plant propagation to produce more transformed plants with the same characteristics and/or can be used to introduce the same characteristic in other varieties of the same or related species.

Furthermore, the characteristic of the transgenic plants of the present invention to maintain normal/rapid/high growth rates under environmental stress conditions can
15 be combined with various approaches to confer environmental stress tolerance with the use of other stress tolerance genes. Some examples of such stress tolerant genes are provided in Holmberg and Bülow (1998). Most prior art approaches which include the introduction of various stress tolerance genes have the drawback that they result in reduced or abnormal growth (compared to non-transgenic controls) under normal,
20 non-stressed conditions, namely stress tolerance comes at the expense of growth and productivity (Kasuga et al., 1999). This correlation between constitutive expression of stress-responsive genes and reduced growth rates under normal growth conditions indicates the presence of cross talk mechanisms between stress response control and growth control.

Furthermore, the characteristic of the transgenic plants of the present invention to display tolerance to environmental stress conditions can be combined with various
25 approaches to confer to plants other stress tolerance genes, e.g., osmotic protectants such as mannitol, proline; glycine-betaine, water-channeling proteins, etc. Thus, the approach of the present invention to confer tolerance to environmental stress
30 conditions to plants can be combined with prior art approaches which include introduction of various stress tolerance genes. Combination of these approaches may have additive and/or synergistic effects in enhancing tolerance or resistance to environmental stress.

Thus, it is immediately evident to the person skilled in the art that the method of
35 the present invention can be employed to produce transgenic stress tolerant plant with

any further desired trait (see for review TIPTEC Plant Product & Crop Biotechnology 13 (1995), 312-397) comprising:

- (i) herbicide tolerance (DE-A 3701623; Stalker (1988)),
- (ii) insect resistance (Vaek (1987)),
- 5 (iii) virus resistance (Powell (1986), Pappu (1995), Lawson (1996)),
- (iv) ozone resistance (Van Camp (1994)),
- (v) improving the preserving of fruits (Oeller (1991)),
- (vi) improvement of starch composition and/or production (Stark (1992), Visser (1991)),
- 10 (vii) altering lipid composition (Voelker (1992)),
- (viii) production of (bio)polymers (Poirer (1992)),
- (ix) alteration of the flower color, e.g., by manipulating the anthocyanin and flavonoid biosynthetic pathway (Meyer (1987), WO90/12084),
- (x) resistance to bacteria, insects and fungi (Duering (1996), Strittmatter (1995), Estruch (1997)),
- 15 (xi) alteration of alkaloid and/or cardiac glycoside composition,
- (xii) inducing maintaining male and/or female sterility (EP-A1 0 412 006; EP-A1 0 223 399; WO93/25695);
- (xiii) higher longevity of the inflorescences/flowers, and
- 20 (xvi) stress resistance.

Thus, the present invention relates to any plant cell, plant tissue, or plant which due to genetic engineering displays an enhanced tolerance or resistance to environmental stress obtainable in accordance with the method of the present invention and comprising a further nucleic acid molecule conferring a novel phenotype to the plant such as one of those described above.

The present invention also relates to a callus or calli consisting essentially of plant cells as defined here above. Such transgenic calli can be preferably used for the production of secondary metabolites in plant cell suspension cultures.

The present invention also relates to any other harvestable part, organ or tissue or propagation material of the plant as defined here above.

The present invention also relates to the seed of a transgenic plant as defined here above, comprising said recombinant DNA.

The present invention also relates to the use of any isolated polynucleic acid as defined above to produce transgenic plants.

The present invention also relates to the use of a recombinant polynucleic acid as defined above, to produce transgenic plants, preferably transgenic plants having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

5 The present invention also relates to the use of an isolated polynucleic acid as defined above, to produce transgenic callus having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

10 The present invention also relates to probes and primers derived from the genes of the invention that are useful for instance for the isolation of additional genes having sequences which are similar to but differ from any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, but which encode a protein
15 having substantially the same biological activity as a protein having the amino acids sequence of any of SEQ ID NO 2 to 120 (even numbers) by techniques known in the art, such as PCR. The presence of a homologous gene in another plant species can for instance be verified by means of Northern or Southern blotting experiments.

The present invention also relates to the cloning of the genomic counterpart of
20 any of the cDNA sequences as represented in SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121. These genomic counterparts can be selected from a genomic library using these cDNA sequences as a probe. The present
25 invention also relates to the coding region as well as the promoter region of any of said genomic clones.

The term "probe" according to the present invention refers to a single-stranded oligonucleotide *sequence* which is designed to specifically hybridize to any of the polynucleic acids of the invention.

30 The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. Preferably the primer is about 5-50 nucleotides long. The term "target region" of a probe or a primer according to the present invention is a sequence within the polynucleic acid(s) to which the probe or the
35 primer is completely complementary or partially complementary (i.e. with some degree

of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

"Specific hybridization" of a probe to a target region of the polynucleic acid(s) means that the probe forms a duplex with part of this region or with the entire region
5 under the experimental conditions used, and that under those conditions this probe does substantially not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

"Specific hybridization" of a primer to a target region of the polynucleic acid(s) means that, during the amplification step, said primer forms a duplex with part of this
10 region or with the entire region under the experimental conditions used, and that under those conditions the primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

Preferably, the probes of the invention are about 5 nucleotides to about 1 Kb
15 long, more preferably from about 10 to 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics. The probes according to the present invention preferably include parts of the cDNA sequences of any of the polynucleic
20 acids as defined above.

The present invention also relates to a composition comprising a polynucleic acid sequence as defined above, a polypeptide as defined above, a probe as defined above or a primer as defined above.

The present invention also relates to a pharmaceutical or agrochemical
25 composition comprising said polynucleic acid, a polypeptide of the invention as defined above.

The present invention also relates to antibodies specifically reacting with a protein or polypeptide according to the present invention.

The following Examples describe by way of example the tolerance and/or
30 resistance to several environmental stress conditions observed for transgenic plants and yeast overexpressing some of the polynucleic acids according to the present invention. Unless stated otherwise in the Examples, all recombinant DNA techniques are carried out according to standard protocols as described in Sambrook et al. (1989) and in volumes 1 and 2 of Ausubel et al. (1994). Standard materials and methods for
35 plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D.

Croy, jointly published by BIOS Scientific Publications Ltd. (UK) and Blackwell Scientific Publications, UK.

These examples and figures are not to be construed as limiting to any of the embodiments of the present invention as set out above. All of the references
5 mentioned herein are incorporated by reference.

BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Figure 1. *At-DBF2* encodes a functional homolog of the yeast *Dbf2* (A) Comparison of the deduced amino acid sequence of *At-DBF2* with that of yeast *DBF2*. Gaps were introduced to optimize the alignment. Roman numerals above the *At-DBF2* sequence indicate the protein kinase catalytic subdomains defined by Hanks et al. (1988). (B) Complementation of *dbf2*. The *dbf2* mutant S7-4A [*MATa dbf2Δ::URA3 ura3 leu2 ade5 trp1 his7*] (Toyn and Johnston, 1994) (B1) forms swollen pairs of daughter cells (dumbbells) at restrictive temperature (37° C). The defective morphology of the *dbf2* mutant can be complemented by transformation with the pYX112 centromeric plasmid (Ingenius, R&D system) containing the *At-DBF2* cDNA (B2) or *DBF2* (B3); wild type (CG378 strain, *MATa ade5 leu2 trp1 ura3*) (B4). Log phase cultures were shifted from 28°C to 37°C and photographed after 16 hours. After 16 hours, 98% of the S7-4A cells arrested with a dumbbell morphology (B1) whereas 6,1 and 0% of dumbbells were observed in B1, B3 and B4. Strains were kindly provided by (Dr Lindl, Max Planck Institut fur Zuchtforschung, Koln, Germany).

Figure 2. Overexpression of *DBF2* or *At-DBF2* enhances tolerance to osmotic, salt, heat and cold stress. Yeast cells were grown in YPD and cell density was adjusted to OD600 at 2. (1) DY, (2) DY transformed with pYX212 containing *DBF2*, pYX-YDBF2, (3) DY transformed with vector alone or (4) with vector containing *At-DBF2*, pYX-AtDBF2. Serial dilutions were made in step1:10. Ten µl of each dilution was spotted on solid YPD medium (control) supplemented with 2M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) or 4µl H₂O₂ (oxidative stress) and incubated at 28°C or at 42°C (heat stress) or at 4°C (cold stress) for 3 days.

Figure 3. *DBF2* and *At-DBF2* are induced by stress. (a) Northern analysis showing the kinetics of *At-DBF2* induction in plants treated with PEG 6000 20 % and the one of *DBF2* in yeast treated with sorbitol 2M for the time indicated. (b) Northern analysis of *At-DBF2* in 10 day-old-plants grown for 5 hours in control conditions (as described in Verbruggen et al. 1993) (1), at 37°C (2), with PEG 6000 20 % (3), NaCl 1% (4), at 4°C (5) or with 0.4 mM H₂O₂ (6); and of *DBF2* in yeast cells grown for 11/2 hour in YPD (1), at 37°C (2), with sorbitol 2M (3), with NaCl 1.2 M (4), at 4°C (5) or with 0.4 mM H₂O₂ (6). Control of loading has been done with EtBr staining and is shown under each Northern analysis.

(c) Western analysis of At-DBF2 in Arabidopsis. Samples are similar to those analysed in (b). Antibodies used were raised against yeast Dbf2 and kindly provided by Dr L. Leindl (Max Planck Institut für Züchtungsforschung, Köln, Germany).

5 Figure 4. *DBF2* overexpression can suppress *hog1* osmosensitivity. The *hog1* mutant (4) [W303-1A, *MATa*, *hog1Δ::TRP1*] and wild type (W303) (1) were kindly provided by Dr Thevelein (Katholieke Universiteit Leuven, Belgium). The *hog1* mutant was transformed with pYX-YDBF2 (2) or pYX-AtDBF2 (3). Each of the 4 strains was grown for 16 hours in YPD (rich medium), and cell density was adjusted to
10 OD600 at 2. Serial dilutions, 1:10 were made at five consecutive steps. Ten microliter of each dilution was spotted on solid YPD medium (control) or solid YPD medium supplemented with 0,9 M NaCl and incubated at 28°C for 3 days.

 Figure 5. *T-DBF2* (*Nicotiana tabacum* DBF2) is periodically expressed during
15 plant cell cycle. Tobacco *DBF2* expression has been followed in BY2 cells synchronised with aphidicolin (a & b) or with propyzamide (c & d) with *At-DBF2* as probe. The measure of relative rate of DNA synthesis and of the mitotic index, the use of the cell cycle markers *CYCB1.2* and *H4* markers have been previously described (Reicheld et al., 1995). *T-DBF2* transcript levels were quantified from the blots shown
20 in b and d using a PhosphorImager (Molecular Dynamics).

 Figure 6. shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left
25 section) upon applying a salt stress of 200 mM NaCl overnight.

 Figure 7 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left
30 section) upon applying an osmotic stress induced by 20% PEG overnight.

 Figure 8 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left

section) upon applying a cold stress by gradually decreasing the temperature until -7°C.

Figure 9 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section) upon applying a heat stress of 2 hours at 48°C.

Figure 10 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section). It can be concluded that the P35S-At-DBF2 transformed plants do not show morphological abnormalities compared to the control transgenic plants.

Figure 11 shows the results of a salt stress tolerance test with transgenic *A. thaliana* plants overexpressing HSP 17.6A (A) or c74 (B). The control plants (bottom left in A and B) is a transgenic line transformed with pBIN-35S-CaMVter. The other sections in A are 5 independently obtained transgenic lines overexpressing HSP17.6A. The other sections in B are 5 independently obtained transgenic lines overexpressing c74.

Figure 12 shows the influence of *At-DBF2* expression in sense and antisense orientations on stress tolerance. BY2 cells were transformed by *A. tumefaciens* with recombinant T-DNA vectors containing *At-DBF2* driven by CaMV 35S RNA promoter, pBIN-35S-*At-DBF2* (upper left and right sections in A or diamonds in B), the CaMV 35S promoter and terminator pBIN-35S-CaMVter (bottom left sections in A or triangles in B), or antisense *At-DBF2* under the control of the CaMV 35S promoter pBIN-35S-AS*At-DBF2* (bottom right sections in A or circles in B). (A) Picture of the same amounts of transgenic cells after 3 weeks of growth on solid medium supplemented with 300 mM NaCl, 25% PEG, 2mM H₂O₂, or at 47°C (heat). (B) Growth of suspension cells in liquid medium. Upon stress, growth was measured as fresh weight and expressed as a percentage of unstressed growth (control) (a). Stresses were applied after subculturing (= day 0) at indicated temperatures (e) and concentrations of NaCl (b) PEG (c), and H₂O₂ (f). For the cold shock (d), cells were maintained at 0°C for 2 days before the 2-week culture at 22°C. For each construction data of three

independent transgenic lines were pooled. To not overload the figure, SDs are not shown (maximum 15% of measured values). (C) Northern analysis of At-DBF2+TDBF2, kin1, and HSP17.6. Total RNAs were extracted from independent lines transformed with pBIN-35S-At-DBF2 (1) and (2), pBIN-35S-CaMter (3), and pBIN-35S-ASAt-DBF2 (4). Osmotic stress was induced with 10% PEG treatment for 5 hr (stressed).

Figure 13 shows the results of the growth of *A. thaliana* plants transformed with p35S-AtHSP17.6A and P35S control (upper right section) upon applying an osmotic stress induced by 20% PEG overnight. The results of two independent experiments are shown, each performed with 3 independently obtained transgenic lines overexpressing At-HSP17.6A (upper left and bottom left and right).

Figure 14 shows the results of the germination of *A. thaliana* plants transformed with p35S-Atc74 and P35S control (bottom section) on mineral medium supplemented with 125 mM NaCl. The results of two independent experiments are shown, each performed with 2 independently obtained transgenic lines overexpressing Atc74 (2 upper sections).

20

Table 1. Classification of the *Arabidopsis thaliana* clones isolated in Example 2. Clones isolated according to the description in example 2 have been analyzed on their potential to confer tolerance. According to the method described in example 2, the tolerance of different yeast transformants expressing an Arabidopsis cDNA to osmotic stress and salt stress was compared with the tolerance of DY wild type cells.

+	:	similar growth to the DY wild type cells;
++	:	growth of the transformant is visible at a 10-fold higher dilution (1:10) than control (1:1);
+++	:	growth of the transformant is visible at a 100-fold higher dilution (1:100) than control (1:1);
++++	:	growth of the transformant is visible at a 1000-fold higher dilution (1:1000) than control (1:1).

Table 2. Exemplary plant-expressible promoters for use in the performance of the present invention.

Table 3. Exemplary stress-inducible promoters for use in the performance of the present invention.

EXAMPLES

Example 1. Construction of the cDNA library.

Total RNA has been isolated from green siliques from *Arabidopsis thaliana* by grinding 1 g of siliques in 4 ml extraction buffer (100 mM tris-HCl, pH 8, 10 mM EDTA, 100 mM LiCl) at 4° C, followed by phenolisation and chloroform: isoamylalcohol (24:1) extraction. To the aqueous phase, LiCl was added up to a final concentration of 2M, and the total RNA was allowed to precipitate overnight at 4°C. After centrifugation, the pellet was redissolved in 400 µl H₂O and reprecipitated with ethanol. Poly(A) messenger RNA was isolated from the total RNA by binding it to an oligo-dT cellulose spun column (Pharmacia), washing the column three times with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 0.5 M NaCl and eluting the mRNA with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA at 65° C.

The eluate was precipitated with ethanol, and cDNA was synthesized using MMLV- reverse transcriptase (Pharmacia) and a d(T)₁₄-XhoI primer for the first strand and *E. coli* DNA polymerase I (Pharmacia) for the second strand.

Example 2. Yeast transformation and selection for osmotolerance.

The cDNA was cloned into pYX vectors (Ingenius, R&D systems; 2 µ based pYX 212 for bank 1, ARS/CEN based pYX112 for bank 2) as EcoRI - XhoI fragments, using an Eco RI/Not I adaptor.

In these constructs, the cDNA is under the control of the strong constitutive TPI promoter. The yeast strain DY (MATa, *his3*, *can1-100*, *ade2*, *leu2*, *trp1*, *ura3::3xSV40AP1-lacZ*; kindly provided by N. Jones, Imperial Cancer Research Fund, London, UK) has been transformed with these cDNA libraries, using the Lithium Acetate transformation procedure (Gietz and Schietsl, 1995). After transformation with the *Arabidopsis* cDNA bank, transformants have been selected for the ability to grow in the presence of 100mM LiCl in a stepwise selection (Lee et al., 1999). LiCl is commonly used for salt tolerance screening in yeast (Haro et al. 1991). Several *A. thaliana* genes, conferring osmotolerance to the yeast, have been isolated (Table 1). To further analyse the potential of the selected *Arabidopsis* cDNA's to confer tolerance to environmental stress in yeast, each yeast transformant expressing such selected *Arabidopsis* cDNA's has been exposed to osmotic stress and salt stress. Each of the transformants was therefore grown for 16 hours in YPD (rich medium), and cell density was adjusted to OD₆₀₀ at 2. Serial dilutions, 1:10, were made at three consecutive

steps. Ten microliters of each dilution was spotted on solid YPD medium (control) supplemented with 2 M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) and incubated at 28°C for 3 days. The results of this drop growth test (see also Lee et al., 1999) are shown in Table 1.

5

Example 3. Characterization of *At-DBF2*.

At-DBF2, a 1.8 kb cDNA (SEQ ID NO 1) has been identified in this screening that encodes a predicted 60.2 kDa protein showing 81 % similarity with the yeast Dbf2 transcriptional regulator. Homology (less than 40% similarity) has also been found with the putative Dbf2 homologues in human, *C. elegans* and *Drosophila* (named Ndr for nuclear Dbf2 related, Millward et al. 1995). The *At-DBF2* deduced protein sequence (SEQ ID NO 2) contains the 11 domains of protein kinases (Figure 1A). Amino acids lying between the invariant residues D and N of domain VI do not match the features of serine/threonine specificity (LKPE) defined by Hanks et al. (1988) but the GSPDYIALE peptide in domain VIII does well indicate serine/threonine specificity and *At-DBF2* can complement the yeast *dbf2* mutant (Figure 1B).

In mature *Arabidopsis* plants, *At-DBF2* is expressed in all tested organs. The highest abundance of transcripts has been found in siliques. A Southern analysis in *Arabidopsis*, tobacco and tomato has revealed that *DBF2* seems to be conserved in plants (see Example 13 below). As *At-DBF2* has been identified in a screening for LiCl tolerance, its effect in other stress situations has been tested in yeast (Figure 2).

Example 4. Overexpression of *Arabidopsis* and *Saccharomyces cerevisiae* *DBF2* enhances cold, heat, salt and drought tolerance in yeast.

In order to test whether the effect was specific to the plant gene, the yeast *DBF2* gene has been overexpressed in the same vector. Upon a drop growth test (Figure 2 and Lee et al., 1999). A remarkable enhancement of stress tolerance can be seen at 42°C, during osmotic stress (sorbitol), and after salt and cold treatments in yeast. There is no difference between stress tolerance afforded by the plant or the yeast gene. The enhancement of stress tolerance due to the overexpression of *At-DBF2* or *DBF2* reflects a role for these genes in stress situations. Therefore yeast and *Arabidopsis* plants have been exposed to sorbitol- and PEG-induced osmotic stress. *At-DBF2* as well as *DBF2* is induced rapidly (1 to 2 hours) and transiently upon osmotic stress (Figure 3A). The expression of *At-DBF2* and *DBF2* has been analyzed during other environmental stresses in *Arabidopsis* plants or in yeast cells after the

time corresponding to the highest induction seen in Fig. 3A (Figure 3B). In plant as in yeast, there is a clear induction after heat, salt, osmotic and to a lesser extent after cold, which perfectly correlates with stresses to which the overexpression enhances tolerance. However, many genes are induced upon stress without relevant adaptive
5 role, amongst others because post-transcriptional mechanisms inhibit subsequent translation. Here *At-DBF2* protein amount, as detected by anti-Dbf2 antibodies, clearly increased upon stress (Figure 3C).

**Example 5. Both *At-DBF2* and *DBF2* can functionally complement the
10 *hog1* mutation.**

To investigate a possible interaction between stress signaling pathways and *DBF2*, the salt sensitive *hog1* mutant was transformed with *At-DBF2* and *DBF2*. The *HOG1* MAP kinase pathway regulates osmotic induction of transcription in yeast (Schuller *et al.* 1994). The osmosensitivity of the mutant could be recovered by the
15 overexpression of both *DBF2* and *At-DBF2* (Figure 4).

Example 6. *At-DBF2* is cell cycle regulated.

DBF2 expression is cell cycle regulated where it plays a role in DNA synthesis initiation but also in nuclear division through its association with the CCR4
20 complex (Komarnitsky *et al.* 1998, Johnston *et al.* 1990). This regulation was investigated in plants. A tobacco BY-2 cell line in which the highest level of culture synchronization, compared with other plant cell lines has been achieved so far (Shaul
et al. 1996, Reicheld *et al.* 1995) was used. Stationary phase cells were diluted into fresh medium and treated with aphidicolin (blocking cells in the beginning of the S
25 phase) for 24 hours, then washed. The percentage of synchronous mitosis after release from the aphidicolin block was about 65 % (Figure 5A-B). A 1.6-Kb tobacco *DBF2* homologue (*T-DBF2*) could be detected on Northern blot with the *At-DBF2* as a probe. *T-DBF2* steady-state transcript level clearly oscillates during the cell cycle and is mainly present during S, decreases during G2 until late M from where it increases
30 until a peak in S phase. *T-DBF2* expression occurs clearly before *CYCB1.2* (a marker of G2-M phases), but parallels the one of H4 (a S phase marker) except at the S/G2 transition, where *T-DBF2* transcripts decline earlier, and at the M/G1 transition, where *T-DBF2* expression increases earlier. The use of the cell cycle markers *CYCB1.2* and H4 is described in Reicheld *et al.*

To follow unperturbed G1 and S phases, BY2 cell suspension was synchronized using a double blocking procedure (Nagata *et al.*, 1992). After the release from the aphidicoline block, cells are treated for 4 hours with propyzamide in the beginning of the preprophase. The percentage of synchronous mitosis after the
5 release from the propyzamide block was higher than 75%. *T-DBF2* was periodically expressed with an undetectable expression until late M, a sharp increase in G1 and a peak in mid S (Figure 5C-D) which confirms results of Figures 5A-B. However a function for the plant *DBF2* in cell cycle can only be assigned with measurement of the kinase activity. In yeast, *DBF2* transcript levels do not correlate with kinase activation
10 which occurs by dephosphorylation (Toyn and Johnson, 1994). The precise function of Dbf2 in regulation of the cell cycle is not known. An essential role has been proposed during anaphase or telophase. No activity has been measured in G1 despite evidence for a role for Dbf2 in initiation of DNA synthesis.

As other proteins recently identified, Dbf2 controls the M/G1 transition
15 which is a major cell cycle transition in yeast (Aerne *et al.* 1998). The existence of a M/G1 control checkpoint has been suggested in plant cells (Hemmerlin and Bach 1998) but its importance compared to G1/S and G2/M has not been investigated.

Overexpression of *DBF2* in yeast results in kinase activity throughout the cell cycle, which may be due to the saturation of a post-translational deactivating
20 mechanism (Toyn and Johnston, 1994). Overexpression of the functionally conserved *At-DBF2* has most probably the same effect. However, the presence of Dbf2 kinase activity at the wrong time in the cell cycle does apparently not affect its progression. In marked contrast constitutive activity has a marked effect on stress tolerance. The role played by *At-DBF2* or *DBF2* in stress is most probably independent from the cell
25 division cycle. *At-DBF2* expression is present in all plant organs (abundant expression is observed in stems where only 1-2 % cells have a mitotic activity) and can be rapidly induced upon stress. However, a link with the cell cycle is not excluded. Higher stress tolerance in yeast overexpressing *DBF2* or *At-DBF2* may be correlated to the overproduction of the kinase in G1 where yeast cells are particularly sensitive to
30 stress. Most plant cells are also thought to be blocked in G1 but the relationship with stress response is poorly known.

Example 7. Tobacco cell transformation and recombinant T-DNA Vector construction

BY2 cells were stably transformed as described (Shaul et al., 1996) by *Agrobacterium tumefaciens* C58C1Rif^R (pGV2260) strain (Deblaere et al., 1985) carrying pBIN-35S-At-DBF2 or pBIN-35S-ASAt-DBF2 recombinant binary vectors. PBIN-35S-At-DBF2 is the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp reporter gene was replaced with a BamHI-SacI fragment containing the At-DBF2 cDNA from pYX-At-DBF2. p-Bin-35S-CaMVter is the plant binary vector pBIN19 in the HindIII-SacI restriction sites of which the hindIII-SacI fragment of pDH51 containing the cauliflower mosaic virus (CaMV) 35S RNA promoter and terminator was cloned. pBIN-35S-ASAt-DBF2 is the pBIN-35S-CaMVter vector in which the At-DBF2 cDNA was cloned in the antisense orientation from pYXAt-DBF2 in the BamHI-SmaI restriction sites, between the CaMV 35S RNA promoter and terminator. More details are described in Lee et al. (1999).

Example 8. Overexpression of At-DBF2 sense and antisense RNA in plant cells

Transgenic plant cells overexpressing *At-DBF2* were generated to test the role of this protein in stress tolerance *in planta*. Tobacco BY2 cells were stably transformed by *A. tumefaciens* carrying the *At-DBF2* cDNA driven by the strong constitutive CaMV 35S RNA promoter. The antisense *At-DBF2* RNA also was overexpressed under the control of the same promoter. Control lines were obtained by transforming tobacco BY2 cells with pBIN-35S-CaMVter. Three independently obtained *At-DBF2*-overexpressing tobacco transgenic cell lines have been selected with a high and similar *At-DBF2* expression and analysed further. Three tobacco transgenic cell lines overexpressing antisense *At-DBF2* were chosen that showed an undetectable tobacco DBF2 transcript level. Both the overexpression of *At-DBF2* and the down-regulation of the endogenous gene by the antisense strategy did not result in significant differences in growth after 2 weeks (Fig. 12A and 12B). On the contrary, marked differences in growth were observed after a 2-week treatment with NaCl, PEG-induced drought, cold, or high temperatures. Transgenic lines that overexpressed *At-DBF2* were clearly more tolerant than control lines. Inhibition of the endogenous DBF2 expression was correlated with a higher sensitivity to those stresses. To understand the basis of stress

tolerance in *At-DBF2*-overexpressing plant cells, expression of stress-induced genes was followed in control and stress conditions (Fig. 12C). Tobacco kin1 and HSP17.6A homologues already were induced in *At-DBF2*-overexpressing tobacco cells in control conditions to a level similar to that observed during stress conditions (PEG-induced drought), suggesting that *At-DBF2* overexpression may mimic a stress signal.

Example 9. Arabidopsis transformation and recombinant T-DNA vector construction with genes conferring tolerance to environmental stress

Arabidopsis were stably transformed as described in Clarke, Wei and Lindsey (1992) by *Agrobacterium tumefaciens* C58C1Rif^R (pGV2260) strains carrying pBIN-35S-*At-DBF2*, pBIN-35S-*At-HSP17.6A*, pBIN-35S-*At-c74* recombinant binary vectors. pBIN-35S-*At-DBF2* is described in Lee et al. 1999. pBIN-35S-*At-HSP17.6A* recombinant binary vector was constructed as following: the EcoRI-XhoI fragment containing *At-HSP17.6A* cDNA in pYX-HSP17.6A (recombinant pYX212) was first cloned in pYES2 (Invitrogen) resulting in pYES-HSP17.6A. Then the BamHI-SphI fragment of pYES-HSP17.6A containing the *At-HSP17.6A* cDNA was cloned in the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp receptor gene was deleted and replaced by the *At-HSP17.6A* cDNA. The 3' protruding ends generated by SacI and SphI were blunt ended by T4 DNA polymerase. pBIN-35S-*c74* was constructed with a similar strategy as pBIN-35S-*AtHSP17.6A* with an intermediary pYES-*Atc74* vector. The *At-c74* cDNA was first amplified with PCR using the primers 5' AAA AAA CAC ATA CAG GAA TTC 3' (SEQ ID NO 122) and 5' AGT TAG CTA GCT GAG CTC GAG 3' (SEQ ID NO 123), then cloned "blunt ended" in the vector pYES2 cut with NotI and BstXI and blunt ended with T4 DNA polymerase. Subsequently, the BamHI-SphI fragment of pYES-*c74* was cloned in pBINm-gfp4 as explained supra.

Example 10. Tolerance to environmental stress in plant cells

Transgenic calli were isolated from each of the transgenic Arabidopsis lines transformed with *At-DBF2*, *At-HSP17.6A* and *At-c74*. The growth of these transgenic calli during salt stress was measured and compared with control calli derived from transgenic Arabidopsis lines transformed with pBIN-35S-CaMVter. Callus pieces (25 for each transgenic line) of similar fresh weight (50 to 100 mg) were therefor grown on callus inducing medium (Clarke et al., 1992) supplemented with 200mM NaCl. After two weeks, from visual inspection, it was clear that transgenic calli transformed with

At-DBF2 or At-HSP17.6A or At-c74 looked much better than control transgenic calli transformed with pBIN-35S-CaMVter. The latter calli turned yellow and started dying. To confirm the observation, the fresh weight of the calli was measured. In comparison with the control transgenic calli, the fresh weight of the transgenic calli was for each of the three lines at least five times higher than the fresh weight of the control transgenic calli.

Example 11. Tolerance to environmental stress in plants.

Seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, p-BIN-35S-At-c74, or pBIN-35S-At-HSP17.6A, were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-AS+At-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 200 mM NaCl for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2 or At-HSP17.6A or At-c74 survived very well (Figure 6 and Figure 11).

To further evaluate the scope of protection to environmental stress, transgenic plants were exposed to osmotic stress. Therefore seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, pBIN-35S-At-c74 or pBIN-35S-At-HSP17.6A were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark,

70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 20 % polyethylene glycol for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2, At-HSP17.6A or At-c74 survived very well (see Figure 7 and 13). Their growth was comparable to growth on control medium without polyethylene glycol.

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to high and low temperatures. Therefor seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, for the experiments with high temperature stress, plants were exposed to 48°C for two hours. For the experiments with low temperature stress, plants were exposed to gradually decreasing temperatures, down to -7°C. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium.

Under both low temperature and high temperature stress, the growth of control transgenic plants was inhibited and eventually they died. The transgenic lines transformed with At-DBF2 or At-c74 survived very well. Their growth was comparable to growth under control conditions with normal temperature (see Figure 8 and 9).

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to salt stress during germination. Sterilized mature seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were placed on top of petri dishes containing MS (Murashige and Skoog) medium with 0,8 % agar and 30 g l⁻¹ sucrose. Control plants were the ones transformed with pBIN-35S-CaMVter. Prior to germination and pH 5.7 adjustment, NaCl was added to a final concentration of 125 mM. Three petri dishes with a mean of 40-50 seeds per dish were used per treatment in every experiment. The complete experiment was repeated

twice. Seed germination at 22°C was followed. Seeds were considered to germinate after radical and green cotyledon emergency occurred.

On control medium (without 125 mM NaCl), germination of all transgenic lines was very similar to each other and to wild type plants. On medium supplemented with 125 mM NaCl, seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate significantly better than control transgenic lines. Less than 10 % of the seeds from transgenic lines transformed with pBIN-35S-CaMVter germinate under these conditions. In contrast, more than 70 % of the seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate on medium containing 125 mM NaCl (Figure 14).

Example 12. Southern hybridisation of At-DBF2 genes in other plants

To investigate whether *DBF2* homologues exist in other plant species, a Southern hybridisation analysis was performed using the full length *At-DBF2* as a probe. Genomic DNA was extracted from tobacco, tomato and rice according to Dellaporta et al. (1983) and further purified by phenol:chloroform extractions.

DNA (10 µg) was digested with restriction enzymes and separated on 1% (w/v) agarose gels using Lambda DNA digested with Hind III as molecular size standards. The DNA was transferred on to nylon membranes (Hybond N; Amersham, little Chalfont, UK) in 0.4 N NaOH. Filters were UV-cross-linked for 30 seconds, prehybridized for 3 hours at 56°C in hybridization solution (2x SSPE, 0.1%(w/v) SDS, 5x Denhardt solution) using 200 gm⁻³ denatured salmon sperm DNA, and hybridized overnight with radiolabelled probes. 1X SSPE was 0.15 M NaCl/ 0.01 M sodium dihydrogen phosphate/ 1 mM EDTA

Filters were washed at 56°C in 2x SSPE, 0.1% (w/v) SDS for 20 min, then 1x SSPE, 0.1% (w/v) SDS for 20 min, and finally in 0.1x SSPE, 0.1% (w/v) SDS for 20 min. Filters were exposed to X-ray film (Kodak X-AR; Kodak, NY, USA) in the presence of intensifying screens for 24 hours.

The results of the hybridisation experiments show that tobacco, tomato and rice have at least one homologue to At-DBF2.

Tabel 1

putative function in	Features of encoded protein	SEQ ID NO.	Growth on medium with 1,2 M NaCl	growth on medium with 2,0 M sorbitol
signalling	Similar to a yeast DBF2 cell cycle protein	1	++++	++++
metabolism	HSP17.6A	3	++++	++++
unknown	C74	5	+++	+++
metabolism	Similar to ADH2	7	+	++++
metabolism	Similar to D. melanogaster catalase/catalase 3	9	++++	+
metabolism	Similar to the HSP90 heat shock protein family	11	++++	++++
metabolism	similar to phosphoenolpyruvate carboxylase	13	+	+++
metabolism	pathogen related proteins, class 10	15	+	++++
metabolism	Arabidopsis ascorbate peroxidase	17	++++	++++
metabolism	similar to phosphatase binding protein	19	++++	++++
metabolism	similar to phosphatase binding protein	21	++++	++++
metabolism	similar to retinol dehydrogenase	23	+++	++++
metabolism	similar to retinol dehydrogenase	25	++++	++++
metabolism	ribosomal protein	27	++++	++++
metabolism	ribosomal protein	29	++++	++++
metabolism	similar to a protein transporter (kinase homolog)	31	++++	++++
metabolism	similar to a peptide transporter	33	++++	+
metabolism	similar to a wheat low affinity cation transporter LCT1	35	++++	++++
metabolism	similar to yeast iso-1-cytochrome c (CYC-1)	37	++++	++++
metabolism	similar to yeast OSM1	39	++++	++++
metabolism	similar to yeast copper uptake gene (CUP1)	41	++++	+++
metabolism	similar to yeast UV-induced damage repair protein (RAD7)	43	++++	++++
metabolism	electron transporter, apocytochrome b	45	++++	++++
metabolism	similar to membrane lipoprotein LPPL1	47	++++	++++
metabolism	similar to tobacco auxin binding protein	49	+	++++
metabolism	similar to tobacco cytokinin binding protein CBP 57	51	+++	++++
signalling	similar to calcium binding protein yeast calcineurin B	53	+++	++++

signalling	similar to calcium binding protein glycine max calnexin	55	++++	+++
signalling	similar to calcium binding protein Dictyostelium discoideum calreticulin	57	++++	++++
signalling	similar to calcium binding protein calmodulin 1	59	++++	+
signalling	similar to calcium binding protein calmodulin 2	61	+	++++
signalling	MAP kinase kinase, homologous to Dictyostelium mekA (DdMek1)	63	++++	+++
signalling	similar to human adenosine kinase	65	+	++++
signalling	similar to human tyrosine kinase	67	++++	++++
signalling	similar to common ice plant tyrosine kinase	69	++++	++++
signalling	similar to the yeast protein kinase C receptor	71	++++	++++
signalling	similar to tobacco and Arabidopsis HAT7 homeotic protein	73	++	++++
signalling	similar to E. coli sigma factor regulator (RSEB)	75	+	++++
signalling	similar to human protein phosphatase 2C	77	++++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	79	++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	81	++	++++
metabolism	pathogen related proteins, class 10	83	++++	++++
metabolism	cell wall peroxidase	85	++++	+++
metabolism	ribosomal protein	87	+++	++++
metabolism	salt stress induced protein, SAS 1	89	++++	++++
metabolism	PR gene (AIG2)	91	++++	++++
metabolism	MT1c	93	++++	++++
metabolism	IPP2 (Isopentenyl diphosphate)	95	+++	++++
metabolism	chlorophyll a/b binding protein	97	+++	+++
metabolism	glutathione transferase	99	++	++++
signalling	cold- and ABA inducible, calcium dependent - kinase, Kin1	101	++++	++++
signalling	MAP kinase, Atmpk1	103	++	++++
signalling	Arabidopsis cell cycle protein histone H2A	105	++++	++++
unknown	chromosome 4 - sequence	107	+++	++++
unknown	chromosome 4 - sequence	109	+	++++
unknown	chromosome 5 - sequence	111	++++	+++
unknown	chromosome 5 - sequence	113	++++	++
unknown	chromosome 5 - sequence	115	++++	++++
unknown	chromosome 5 - sequence	117	+	++++
unknown	chromosome 5 - sequence	119	+	++++

signalling	similar to calcium binding protein centrin (caltractin)	121	++++	++++
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TABLE 2
EXEMPLARY PLANT-EXPRESSIBLE PROMOTERS FOR USE IN THE PERFORMANCE OF
THE PRESENT INVENTION

GENE SOURCE	EXPRESSION PATTERN	REFERENCE
α -amylase (<i>Amy32b</i>)	Aleurone	Lanahan <i>et al.</i> (1992); Skriver <i>et al.</i> (1991)
cathepsin β -like gene	Aleurone	Cejudo <i>et al.</i> (1992)
<i>Agrobacterium rhizogenes</i> rolB	Cambium	Nilsson <i>et al.</i> (1997)
PRP genes	cell wall	http://salus.medium.edu/mmj/tierney/html
barley <i>ltr1</i> promoter	Endosperm	
synthetic promoter	Endosperm	Vicente-Carbajosa <i>et al.</i> (1998)
AtPRP4	Flowers	http://salus.medium.edu/mmj/tierney/html
chalcone synthase (<i>chsA</i>)	Flowers	van der Meer <i>et al.</i> (1990)
<i>apetala-3</i>	Flowers	
Chitinase	fruit (berries, grapes, etc)	Thomas <i>et al.</i> CSIRO Plant Industry, Urrbrae, South Australia, Australia; http://winetitles.com.au/gwrdc/csh95-1.html
<i>rbcS-3A</i>	green tissue (eg leaf)	Lam <i>et al.</i> (1990); Tucker <i>et al.</i> (1992)
leaf-specific genes	Leaf	Baszczynski <i>et al.</i> (1988)
AtPRP4	Leaf	http://salus.medium.edu/mmj/tierney/html
<i>Pinus cab-6</i>	Leaf	Yamamoto <i>et al.</i> (1994)
SAM22	Senescent leaf	Crowell <i>et al.</i> (1992)
<i>R. japonicum nif</i> gene	Nodule	United States Patent No. 4, 803, 165
<i>B. japonicum nifH</i> gene	Nodule	United States Patent No. 5, 008, 194

GmENOD40	Nodule	Yang <i>et al.</i> (1993)
PEP carboxylase (PEPC)	Nodule	Pathirana <i>et al.</i> (1992)
Leghaemoglobin (Lb)	Nodule	Gordon <i>et al.</i> (1993)
<i>Tungro bacilliform</i> virus gene	Phloem	Bhattacharyya-Pakrasi <i>et al.</i> (1992)
sucrose-binding protein gene	plasma membrane	Grimes <i>et al.</i> (1992)
pollen-specific genes	pollen; microspore	Albani <i>et al.</i> (1990); Albani <i>et al.</i> (1991)
maize pollen-specific gene	Pollen	Hamilton <i>et al.</i> (1992)
sunflower pollen-expressed gene	Pollen	Baltz <i>et al.</i> (1992)
<i>B. napus</i> pollen-specific gene	pollen; anther; tapetum	Arnoldo <i>et al.</i> (1992)
root-expressible genes	Roots	Tingey <i>et al.</i> (1987); An <i>et al.</i> (1988);
tobacco auxin-inducible gene	root tip	Van der Zaal <i>et al.</i> (1991)
β -tubulin	Root	Oppenheimer <i>et al.</i> (1988)
Tobacco root-specific genes	Root	Conkling <i>et al.</i> (1990)
<i>B. napus</i> G1-3b gene	Root	United States Patent No. 5, 401, 836
SbPRP1	Roots	Suzuki <i>et al.</i> (1993)
AtPRP1; AtPRP3	roots; root hairs	http://salus.medium.edu/mmq/tierney/html
RD2 gene	root cortex	http://www2.cnsu.edu/ncsu/research
TobRB7 gene	root vasculature	http://www2.cnsu.edu/ncsu/research
AtPRP4	leaves; flowers; lateral root primordia	http://salus.medium.edu/mmq/tierney/html
Seed-specific genes	Seed	Simon <i>et al.</i> (1985); Scofield <i>et al.</i> (1987); Baszczyński <i>et al.</i> (1990)
Brazil Nut albumin	seed	Pearson <i>et al.</i> (1992)
Legumin	Seed	Ellis <i>et al.</i> (1988)
Glutelin (rice)	Seed	Takaiwa <i>et al.</i> (1986); Takaiwa <i>et al.</i>

		(1987)
Zein	Seed	Matzke <i>et al.</i> (1990)
NapA	Seed	Stalberg <i>et al.</i> (1996)
Sunflower oleosin	seed(embryo and dry seed)	Cummins <i>et al.</i> (1992)
LEAFY	shoot meristem	Weigel <i>et al.</i> (1992)
<i>Arabidopsis thaliana knat1</i>	shoot meristem	Accession number AJ131822
<i>Malus domestica kn1</i>	shoot meristem	Accession number Z71981
CLAVATA1	shoot meristem	Accession number AF049870
Stigma-specific genes	Stigma	Nasrallah <i>et al.</i> (1988); Trick <i>et al.</i> (1990)
Class I patatin gene	Tuber	Liu <i>et al.</i> (1991)
Blz2	Endosperm	EP99106056.7
PCNA rice	Meristem	Kosugi <i>et al.</i> (1991); Kosugi and Ohashi (1997)

Table 3. Stress inducible promoters

Name	Stress	Reference
P5CS (delta(1)-pyrroline-5-carboxylate syntase)	salt, water	Zhang et al; Plant Science. Oct 28 1997; 129(1): 81-89
cor15a	Cold	Hajela et al., Plant Physiol. 93: 1246-1252 (1990)
cor15b	Cold	Wlhelm et al., Plant Mol Biol. 1993 Dec; 23(5):1073-7
cor15a (-305 to +78 nt)	cold, drought	Baker et al., Plant Mol Biol. 1994 Mar; 24(5): 701-13
rd29	salt, drought, cold	Kasuga et al., Nature Biotechnology, vol 18, 287-291, 1999
heat shock proteins, including artificial promoters containing the heat shock element (HSE)	Heat	Barros et al., Plant Mol Biol, 19(4): 665-75, 1992. Marrs et al., Dev Genet., 14(1): 27-41, 1993. Schoffl et al., Mol Gen Gent, 217(2-3): 246-53, 1989.
smHSP (small heat shock proteins)	heat	Waters et al, J Experimental Botany, vol 47, 296, 325-338, 1996
wcs120	Cold	Ouellet et al., FEBS Lett. 423, 324-328 (1998)
ci7	Cold	Kirch et al., Plant Mol Biol, 33(5): 897-909, 1997 Mar
Adh	cold, drought, hypoxia	Dolferus et al., Plant Physiol, 105(4): 1075-87, 1994 Aug
pws18	water: salt and drought	Joshee et al., Plant Cell Physiol, 39(1): 64-72, 1998, Jan
ci21A	Cold	Schneider et al., Plant Physiol, 113(2): 335-45, 1997
Trg-31	Drought	Chaudhary et al., Plant Mol Biol, 30(6): 1247-57, 1996
Osmotin	Osmotic	Raghothama et al., Plant Mol Biol, 23(6): 1117-28, 1993

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Claims

1. A method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.
2. An isolated polynucleic acid obtainable by a method according to claim 1.
3. The isolated polynucleic acid of claim 2 which encodes a polypeptide as listed in Table 1.
4. The isolated polynucleic acid of claim 3, which is chosen from:
 - (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or the complementary strands thereof;
 - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
 - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
 - (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).
5. The isolated polynucleic acid of any of claim 2 to 4, which encodes a plant homolog of yeast DBF2 kinase.
6. The isolated polynucleic acid of claim 5, which is chosen from:
 - (a) SEQ ID NO 1, or the complementary strands thereof;
 - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

5

7. Use of an isolated polynucleic acid of claims 2 to 3 which encodes an HSP 17.6A protein for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

- 10 8. Use of an isolated polynucleic acid of claim 7 for expression of the protein encoded thereby in a plant cell, with said polynucleic acid being chosen from:

- (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- 15 (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of
- 20 (a) to (c).

9. Use of an isolated polynucleic acid as defined above which is chosen from:

- (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 25 or 119, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 30 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

- 35 for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

10. The isolated polynucleic acid of any of claims 2 to 4, which encodes a c74 protein which is chosen from:

5

- (a) SEQ ID NO 5, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

10

11. An isolated polypeptide encoded by a polynucleic acid according to or as defined in any of claims 2 to 10, or a functional fragment thereof.

15

12. The isolated polypeptide of claim 11 having at least part of the sequence of any of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

20

13. A method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising transiently introducing into a plant cell a recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2 to 10 which is expressed in an amount effective to confer enhanced tolerance or resistance to environmental stress.

25

14. A method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising stably introducing into a plant cell a recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2 to 10 which is expressed in an amount effective to confer enhanced tolerance or resistance to environmental stress.

30

35

15. The method of claims 13 or 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 5 or 6 encoding a plant DBF2 kinase.
- 5
16. The method of claim 16 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 7 or 8 encoding an HSP 17.6A protein.
- 10
17. The method of claim 13 to 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claim 10 encoding a c74 protein.
- 15
18. The method of any of claims 13 to 17, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- a polynucleic acid according to or as defined in any of claims 2 to 10, and,
 - a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 20
19. A method for producing a plant with enhanced tolerance or resistance to environmental stress, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or indirectly increases or induces the activity of a polypeptide of claims 11 or 12, and,
- 25
- 30

- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 5 20. A method of claim 19 wherein said DNA encodes a sense or antisense RNA molecule or a ribozyme capable of increasing or inducing the expression of said endogenous polynucleic acid sequence according to or as defined in any of claims 2 to 10.
- 10 21. A recombinant polynucleic acid comprising:
a polynucleic acid according to or as defined in any of claims 2 to 10, and,
a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 15 22. A recombinant polynucleic acid comprising:
(a) a DNA encoding a protein which when expressed in said plant cell at an effective amount increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or increases or induces the activity of a polypeptide of claims 11 or 12, and,
20 (b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.
23. The recombinant polynucleic acid of claim 22, wherein said DNA encodes an anti-sense RNA, a ribozyme or a sense RNA which when expressed in a cell of a plant
25 increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or which induces or increases the activity of a protein of claim 11 or 12.
- 30 24. The recombinant polynucleic acid of claim 21 comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or part thereof.

25. The recombinant polynucleic acid of claim 21 to 24 comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1.
- 5 26. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a constitutive promoter.
27. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a stress-inducible or organ- or tissue-specific promoter.
- 10 28. The recombinant polynucleic acid of any of claims 21 to 26 wherein said plant-expressible promoter is the 35S promoter of CaMV.
29. A recombinant host cell transformed with at least one isolated polynucleic acid of or as defined in any of claims 2 to 10.
- 15 30. A plant cell transformed with a recombinant polynucleic acid of any one of claims 21 to 28.
31. A plant consisting essentially of plant cells of claim 30.
- 20 32. A callus consisting essentially of plant cells of claim 30.
33. A harvestable part, organ, tissue or propagation material of a plant of claim 31, comprising said recombinant DNA.
- 25 34. The use of a recombinant polynucleic acid of claim 21 to 28 to produce transgenic plants.
- 30 35. A probe which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which hybridizes specifically with said polynucleic acid or the complement thereof.
- 35 36. A primer which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which specifically amplifies said polynucleic acid or the complement thereof.

37. A composition comprising a polynucleic acid sequence of or as defined in any of claims 2 to 10, a polypeptide of claim 11 or 12, a probe of claim 35 or a primer of claim 36.

5

At-DBF2MAGNMSCLSDGHTGTPGGSGHFPNQNLTKRRTRPAGINDSPSPVKCFPPYEDTSNTSLKEVSQPTKYSSNSPPVSPAIFYERATSUCT	89
DBF2	MLSKSEKNVDLLAGNMSNLSFDGHTGTPGGTGLFPNQNLTKRRTRPAGINDSPSPVKPSFFPYEDTSNMDIDEVSQPDMDVSNPKLPPKIFYERATSUKT	100
At-DBF2	QVVSGRAMYFLEYCDMFDYVISRRQRTKQVLEYLQOQSOLPNSDQIKLNEEHSSYLQREHQLSKRRLKPKNRDFEMITQVGGGGYGHVYLARKKDTK	189
DBF2	QVVSVCKMYFLEHYCDMFDYVISRRQRTKQVLEYLQOQSOLPNSDQIKLNEEHSSYLQREHQLSKRRLKPKNRDFEMITQVGGGGYGVYLYARKKDTK	200
At-DBF2	EVCALKILNKKLGLNGTCHVLTERRQSLITTRSETHVKLLSGTTPVSGRGMASELGGDFRTESIGRRCLKSGHARFYISEMFCAVNEKHLST...	287
DBF2	EVCALKILNKKLGLNKGTHVLTERRQSLITTRSETHVKLLSGTTPVSGRGMASELGGDFRTESIGRRCLKSGHARFYISEMFCAVNEKHLST...	300
At-DBF2DSTISNEEDSSINIRLEKFKOLGYPALSEKSIEDRRKLY.....TCPNSMVGSPDYIALEVLGRKRYEYTVDYWS	356
DBF2	LKPENFLIDAKGHIKLTDFGLAAGTISNERIESMKIRLEKIKOLEFPAFTKSTIEDRRKMYNQLREKEINYANSVMGSPDYMALEVLGKDYFTVDYWS	400
At-DBF2	LGCMFLFESLVGYTPFGSGSSTNETYATSRSHKQTLNRARHEDGRAAFYNRTHDLITRHRADLSTRSRFEHEVKMSYFADILFKALRSIIPFPQDSET	456
DBF2	LGCMFLFESLVGYTPFGSGSSTNETYDNLRHWKQTLRRPRQSDGRAAFSDRTWDLITRLIADPINLRSRFEHEVKMSYFADINFSTLRSMIPFPQDSET	500
At-DBF2	DAGYFDDFWNEADIAKYADVFNQCCRTALVDDSAVSSKLVGFTFRHRNGKQGSSGMLFNGLHSDPFSTFY	528
DBF2	DAGYFDDFTSEADMAYADVFKRQDKLTAMVDDSAVSSKLVGFTFRHRNGKQGSSGILFNGLHSDPFSTFY	572

FIGURE 1 A

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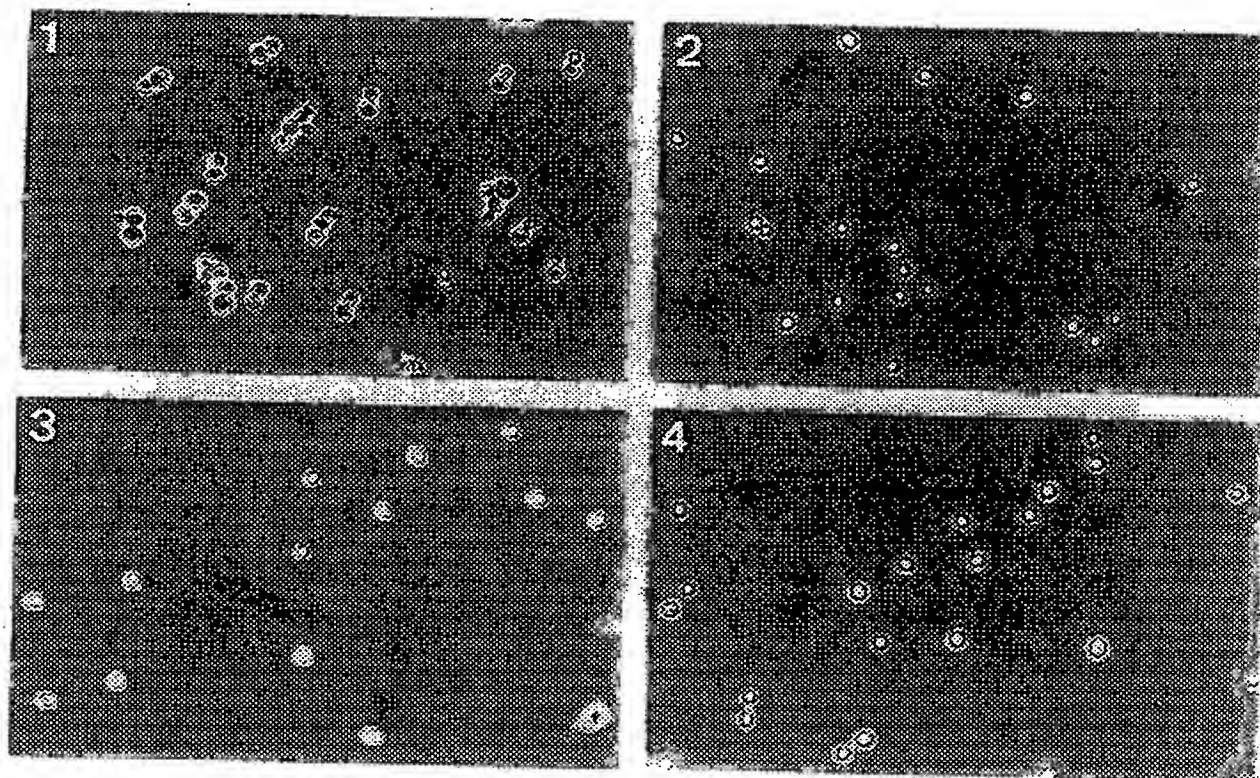


FIGURE 1B

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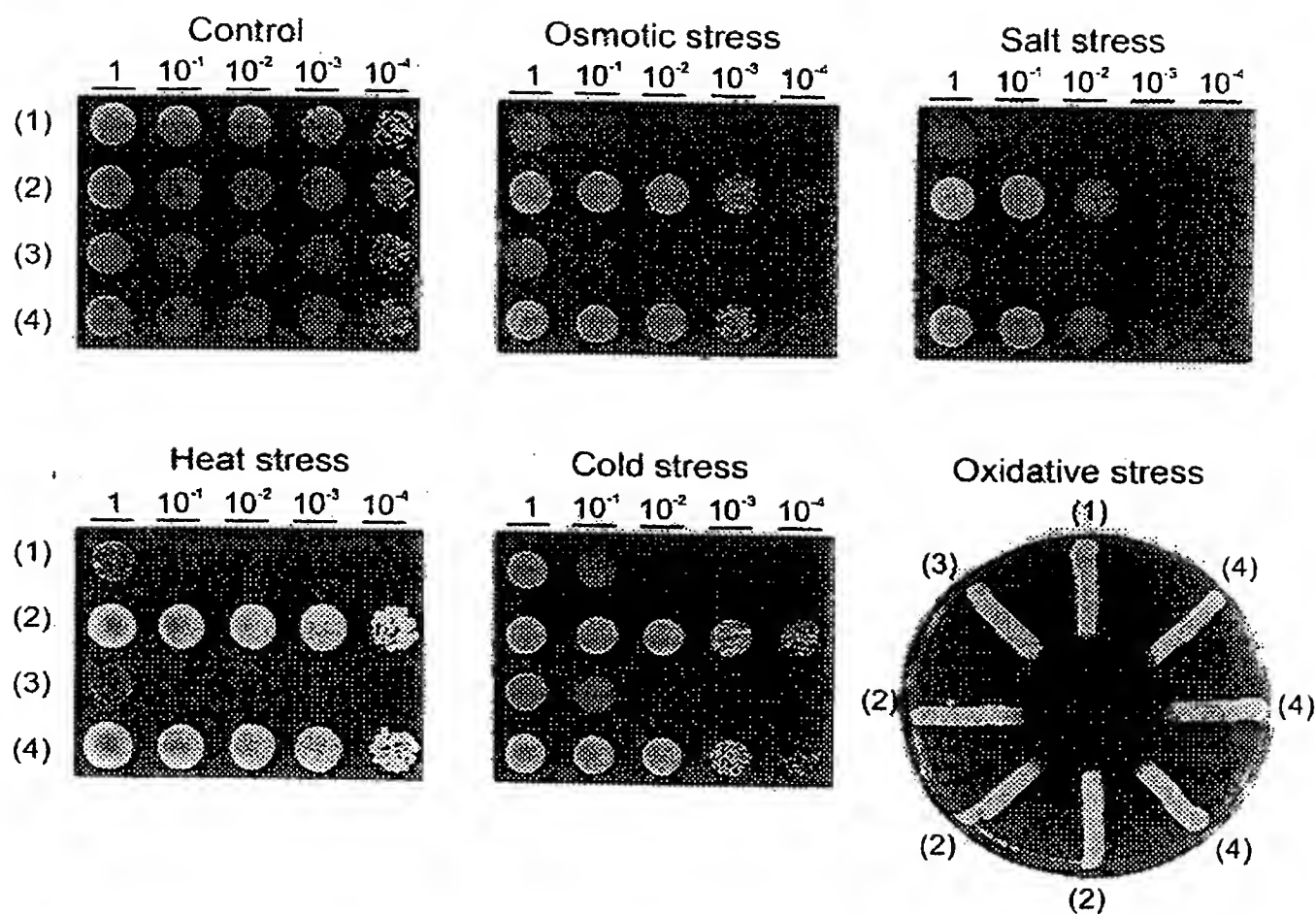


FIGURE 2

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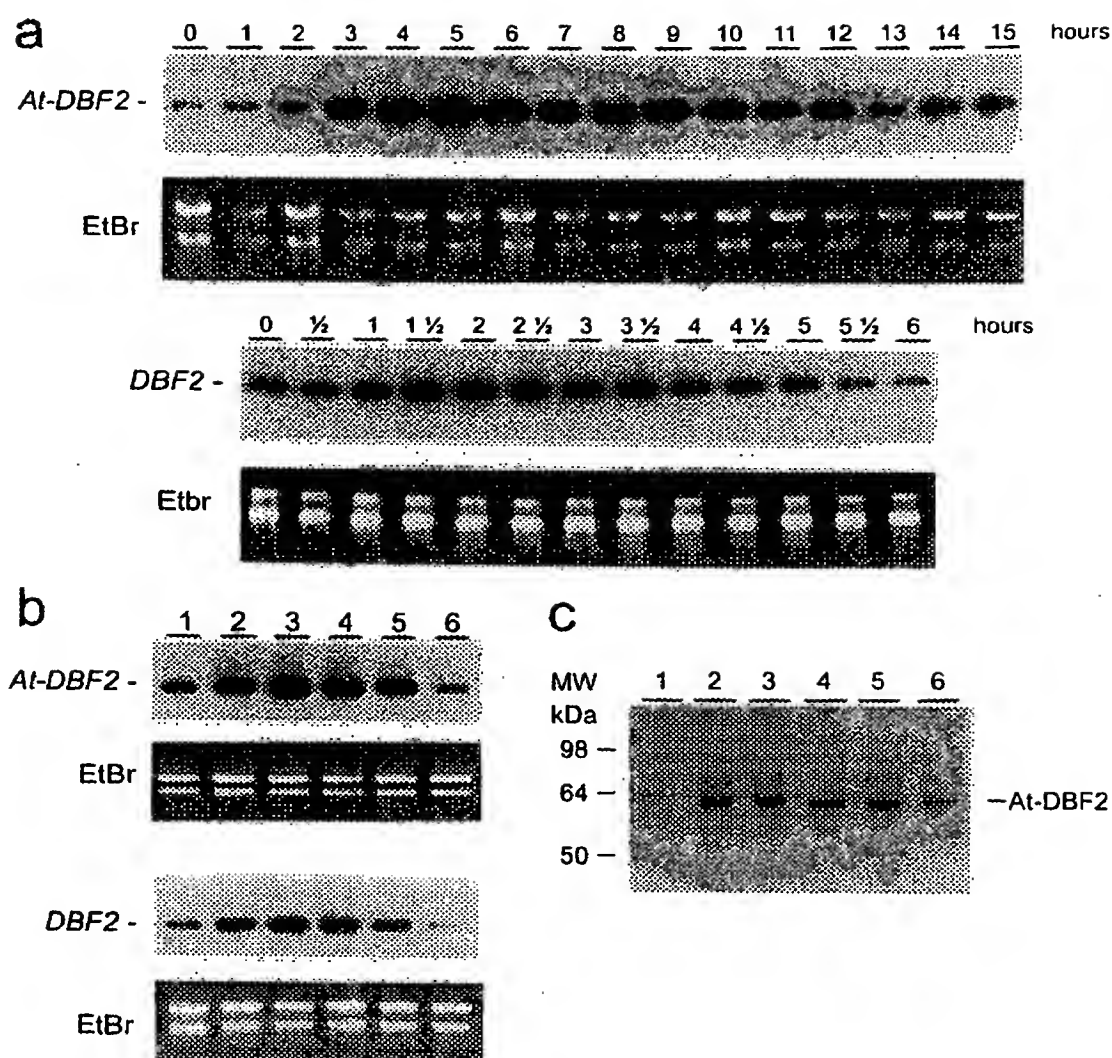


FIGURE 3

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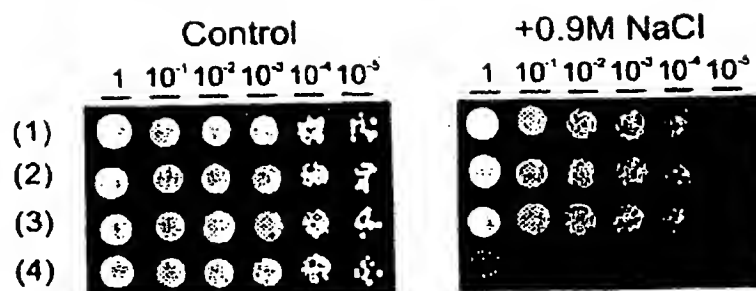


FIGURE 4

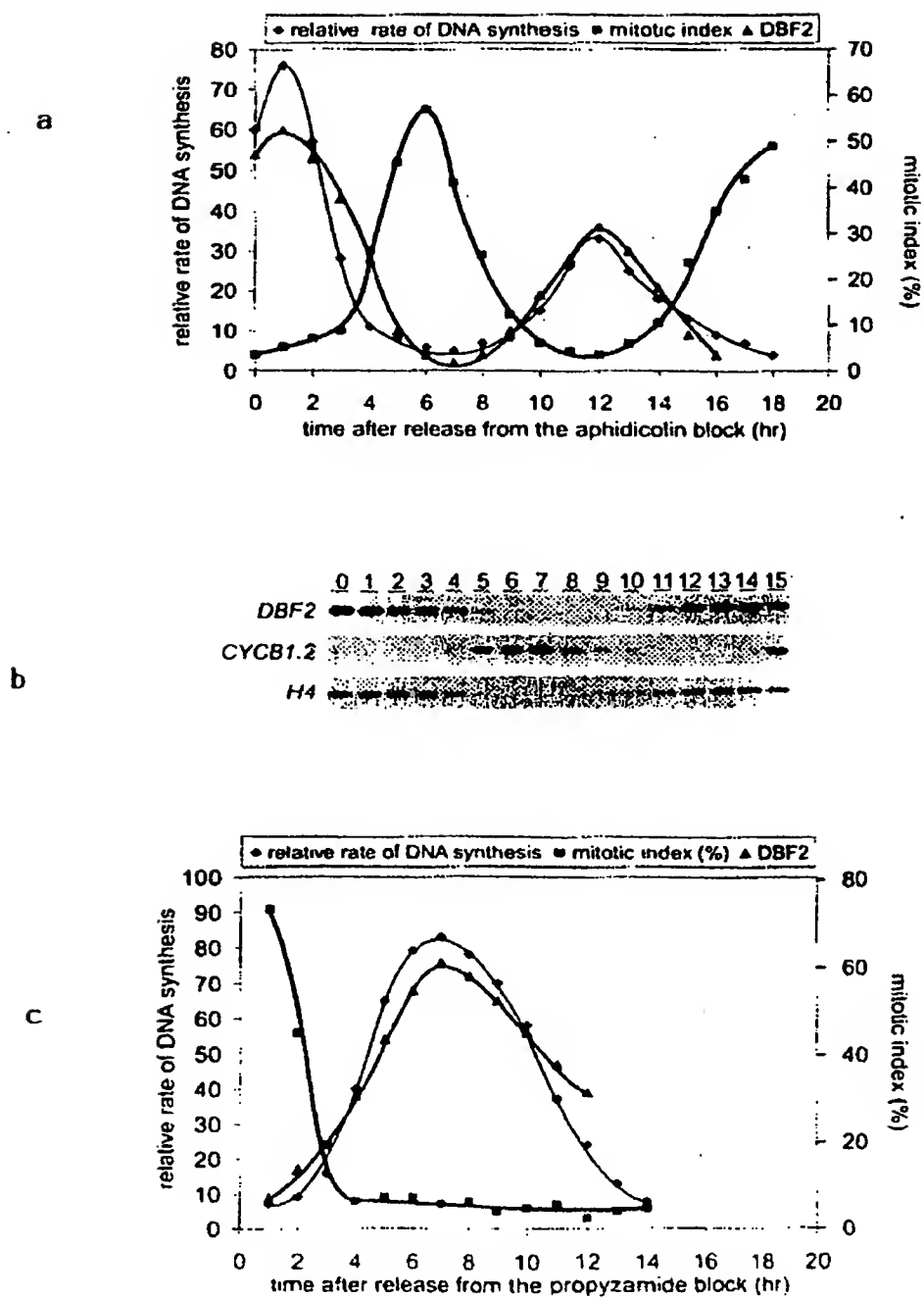


FIGURE 5

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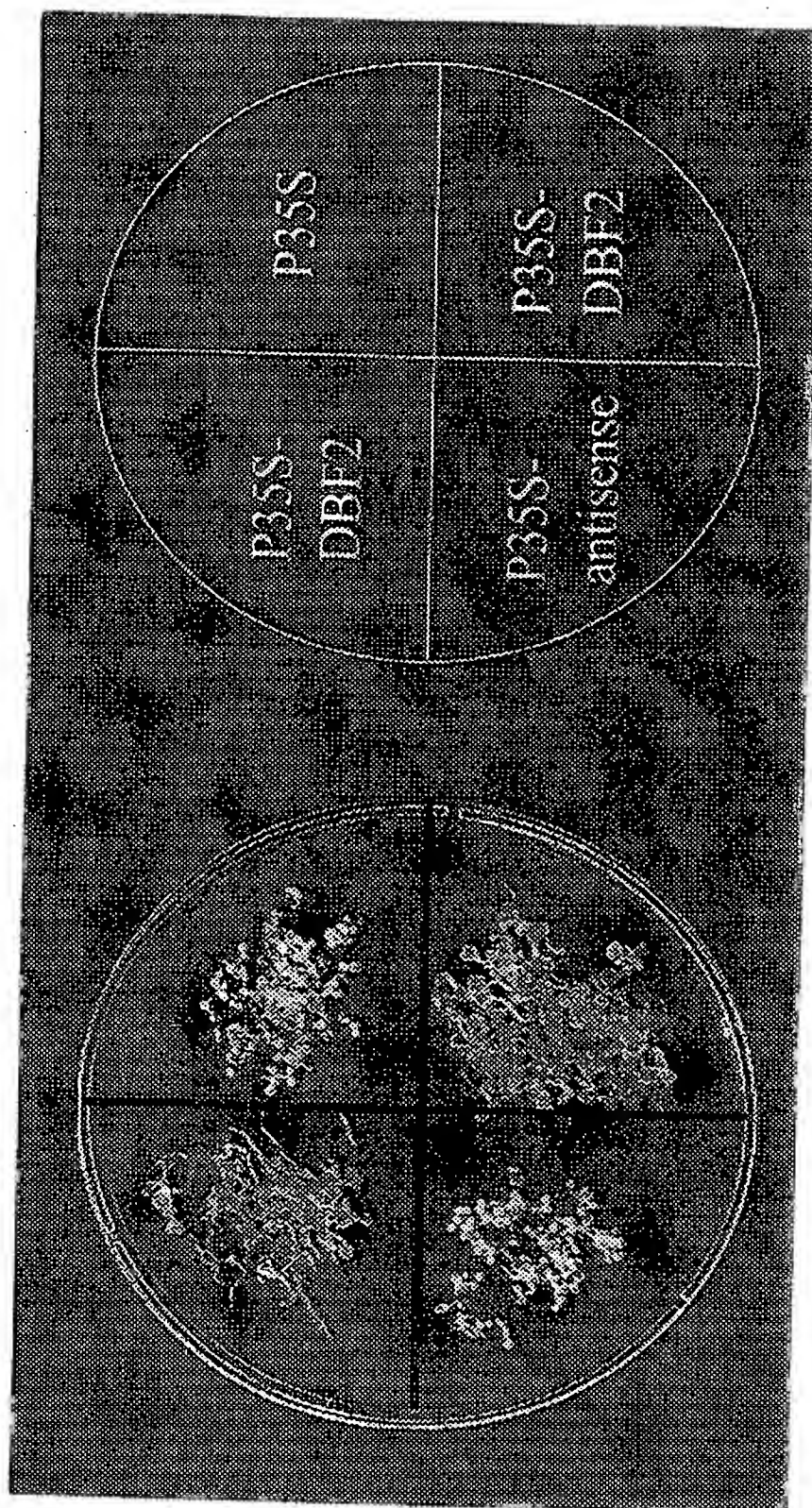


FIGURE 6

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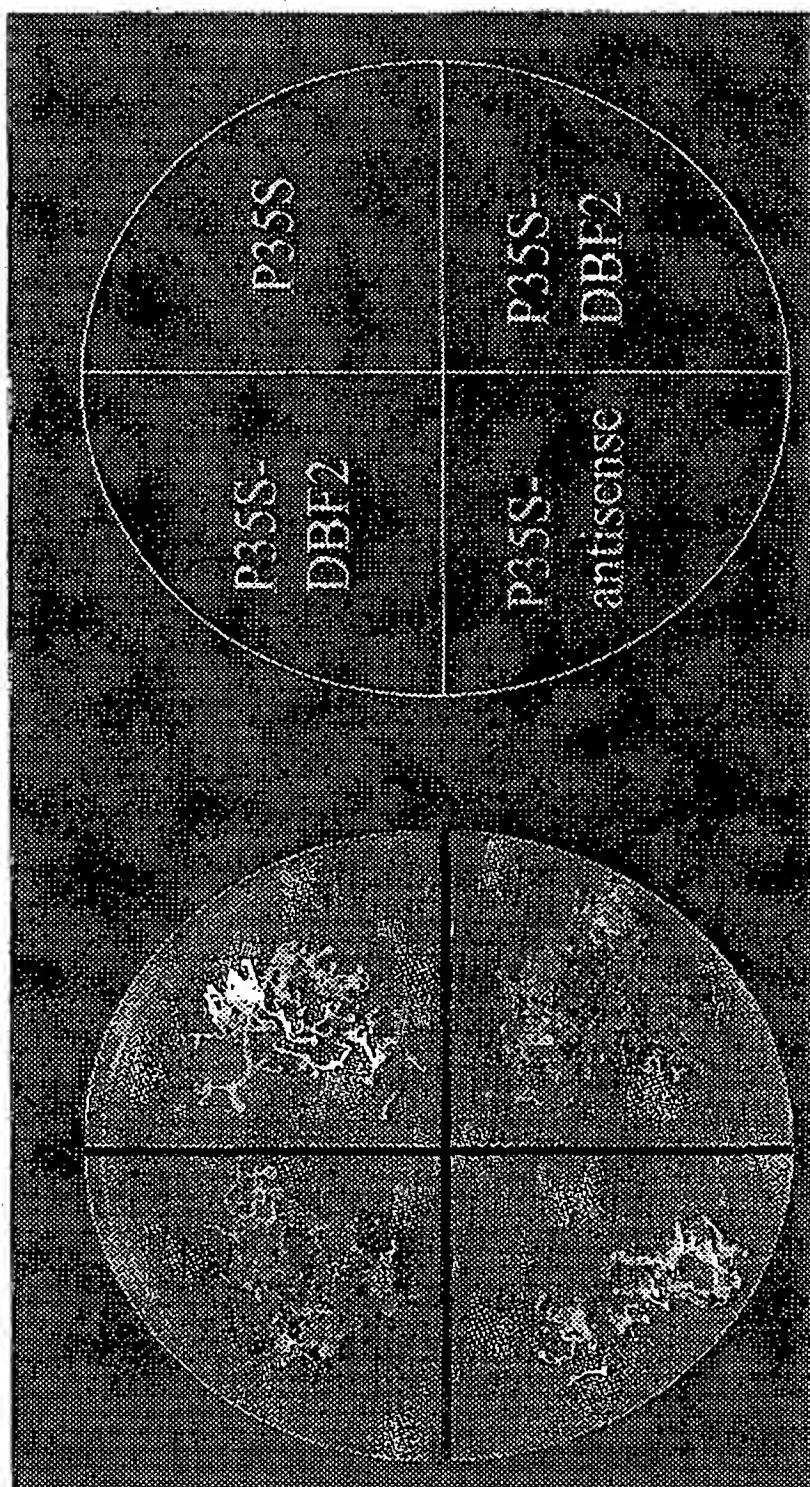


FIGURE 7

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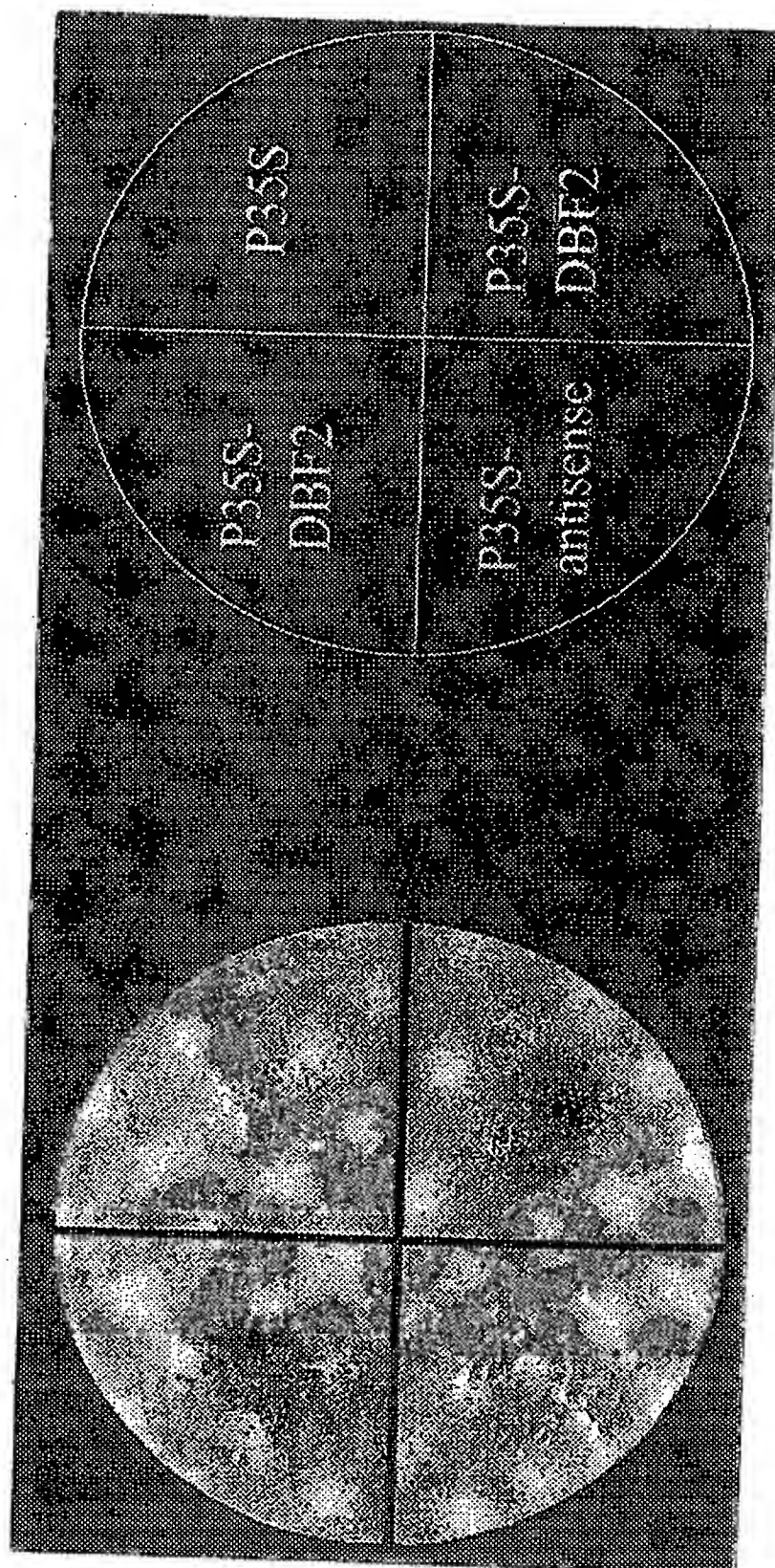


FIGURE 8

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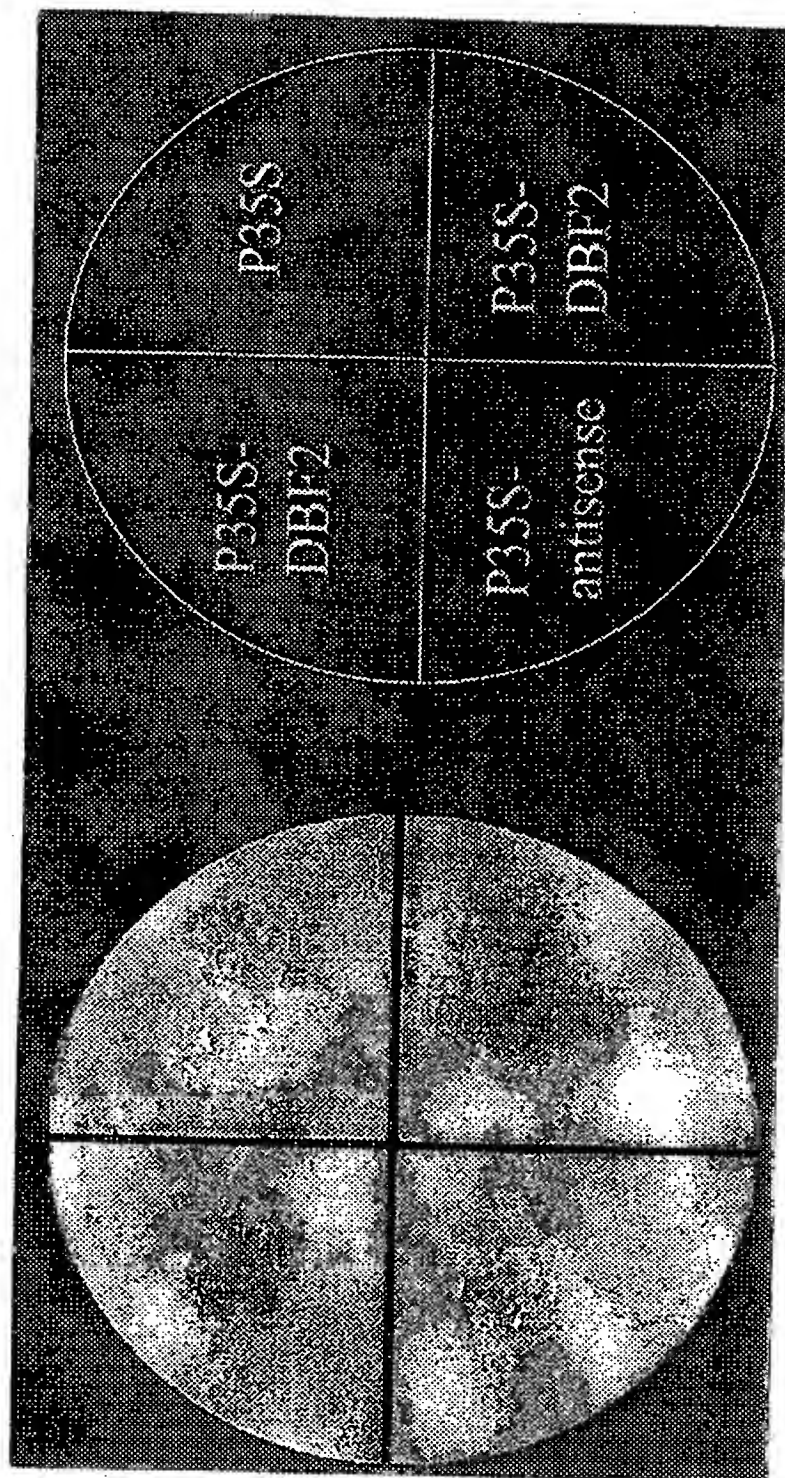


FIGURE 9

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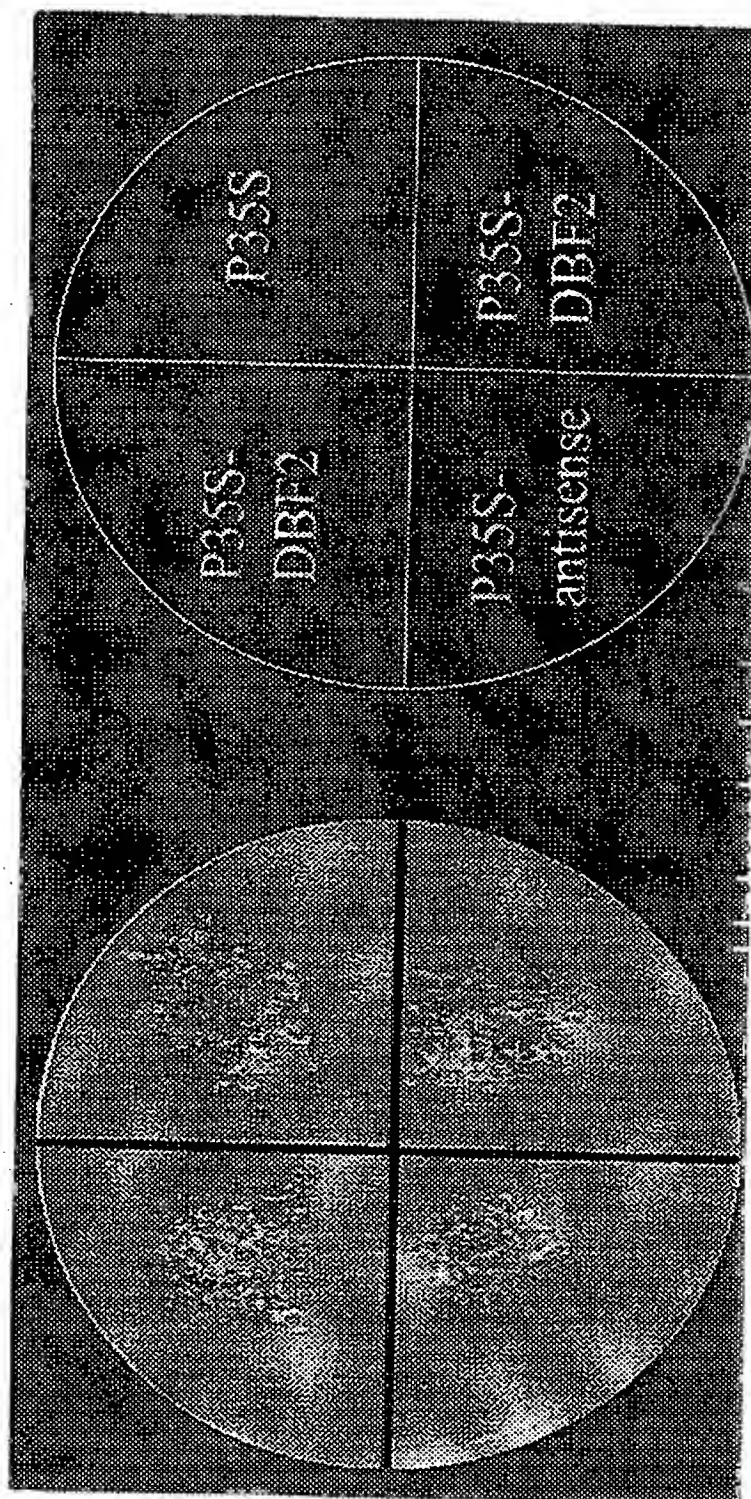


FIGURE 10

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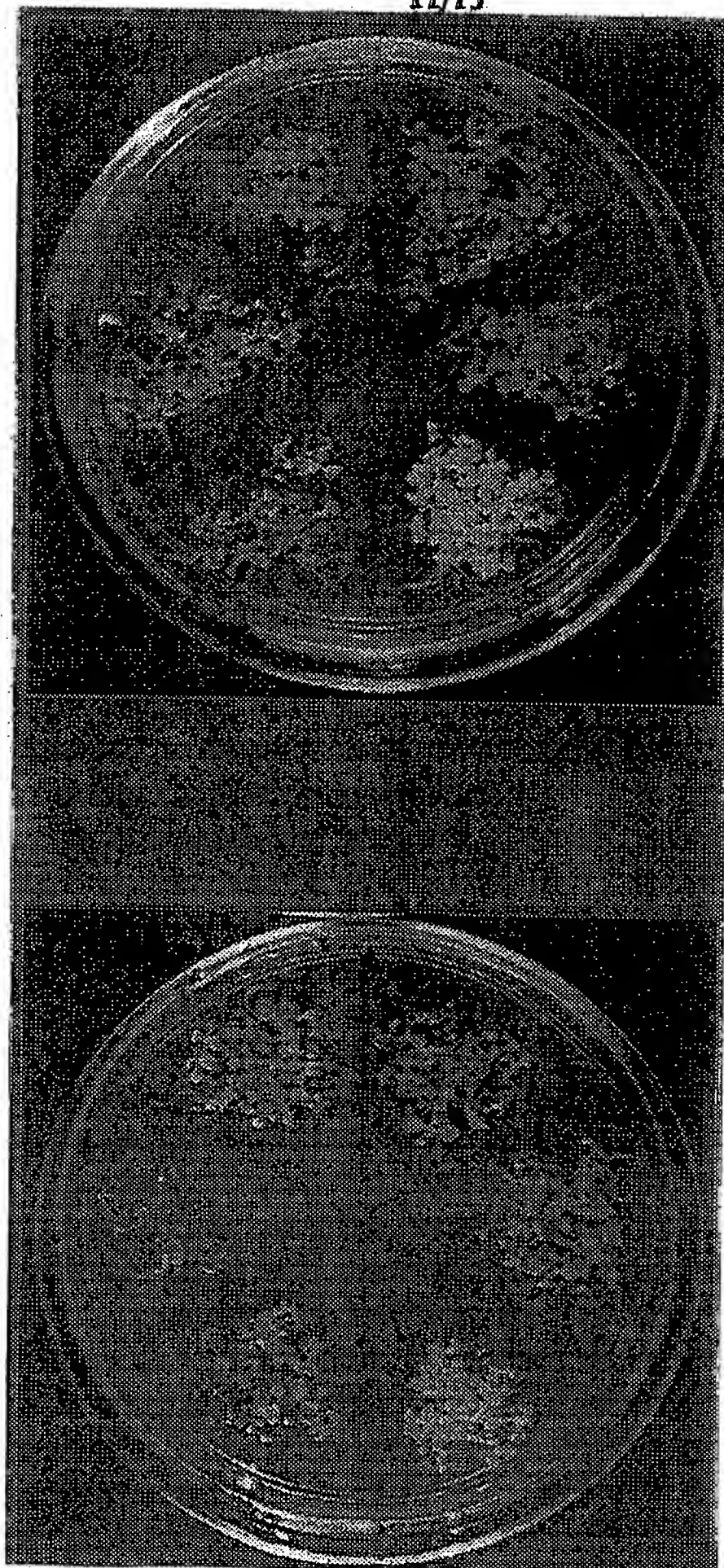


FIGURE 11

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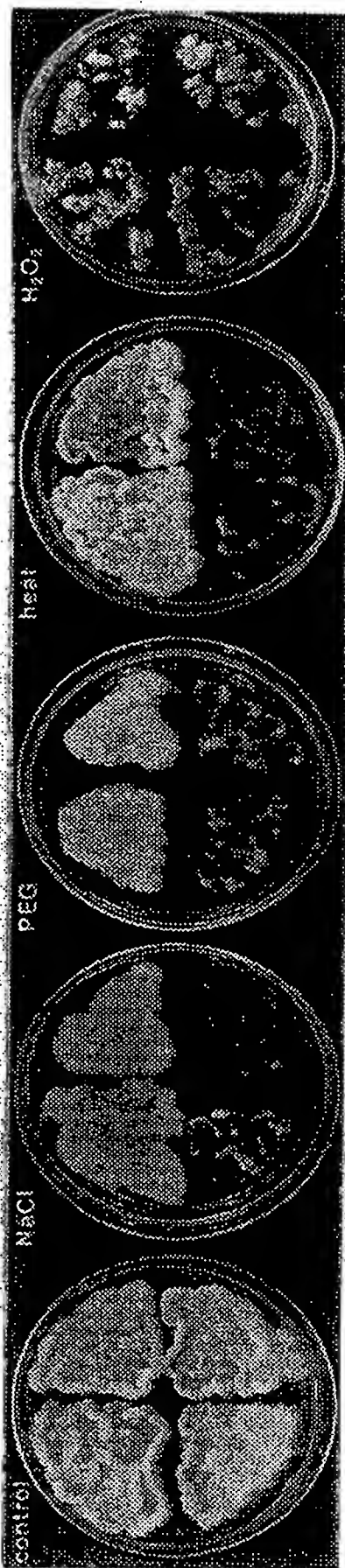


FIGURE 12A

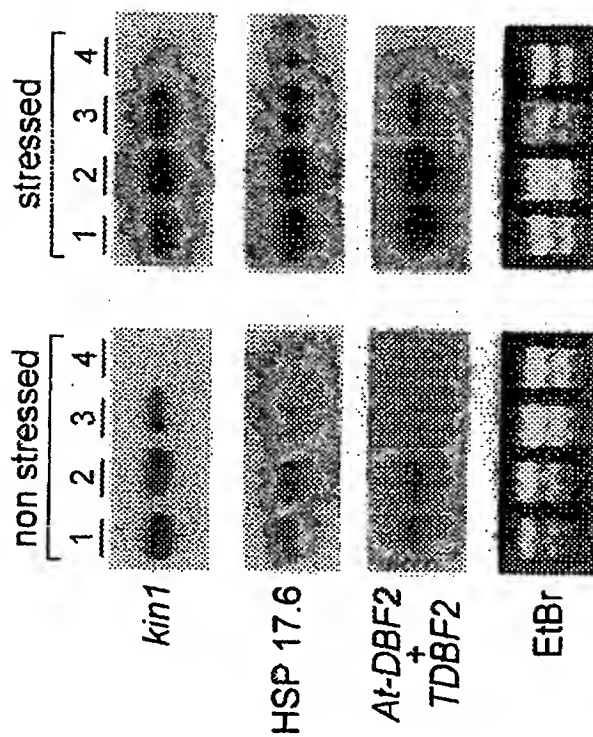


FIGURE 12c

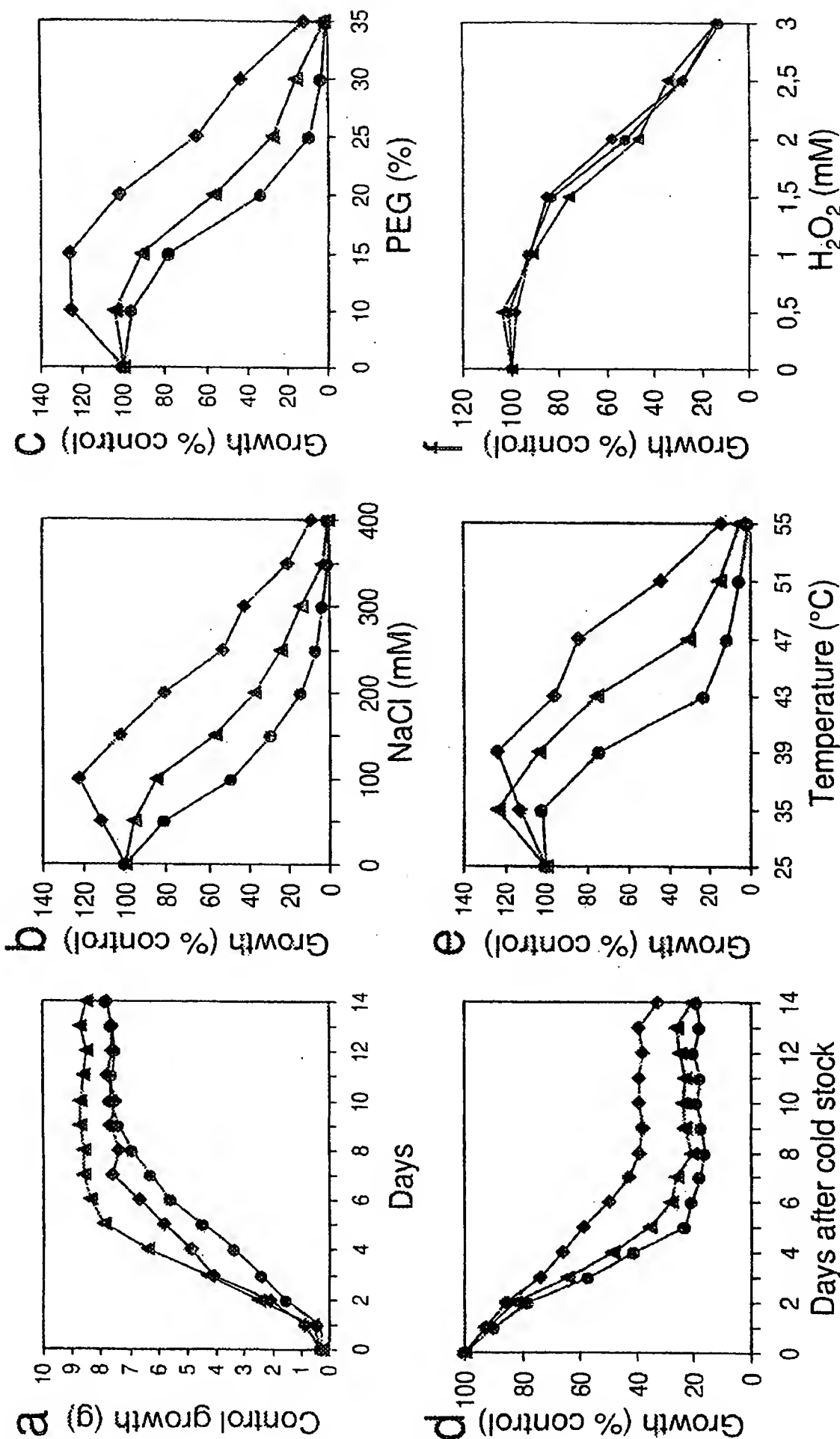


FIGURE 12B

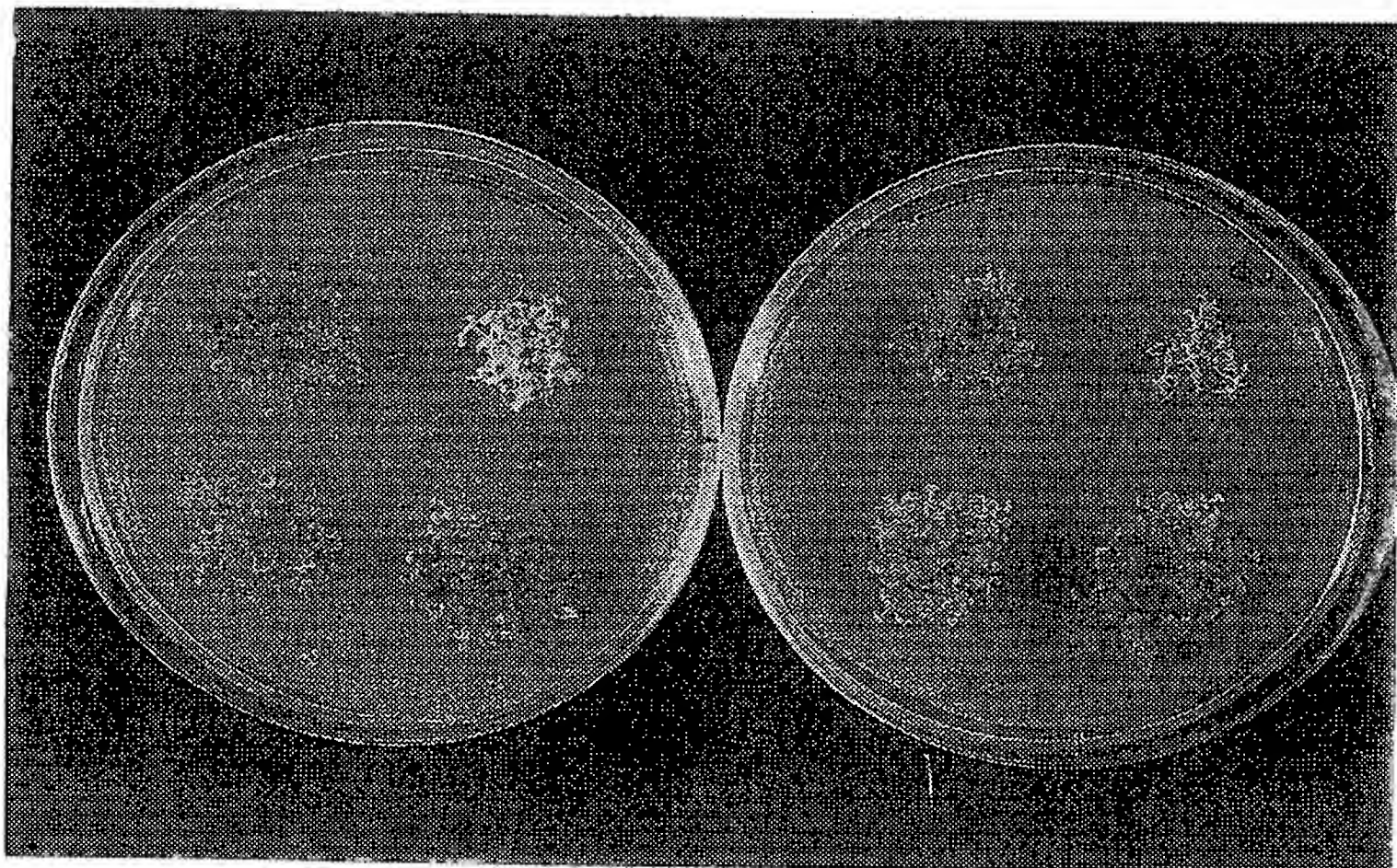


FIGURE 13

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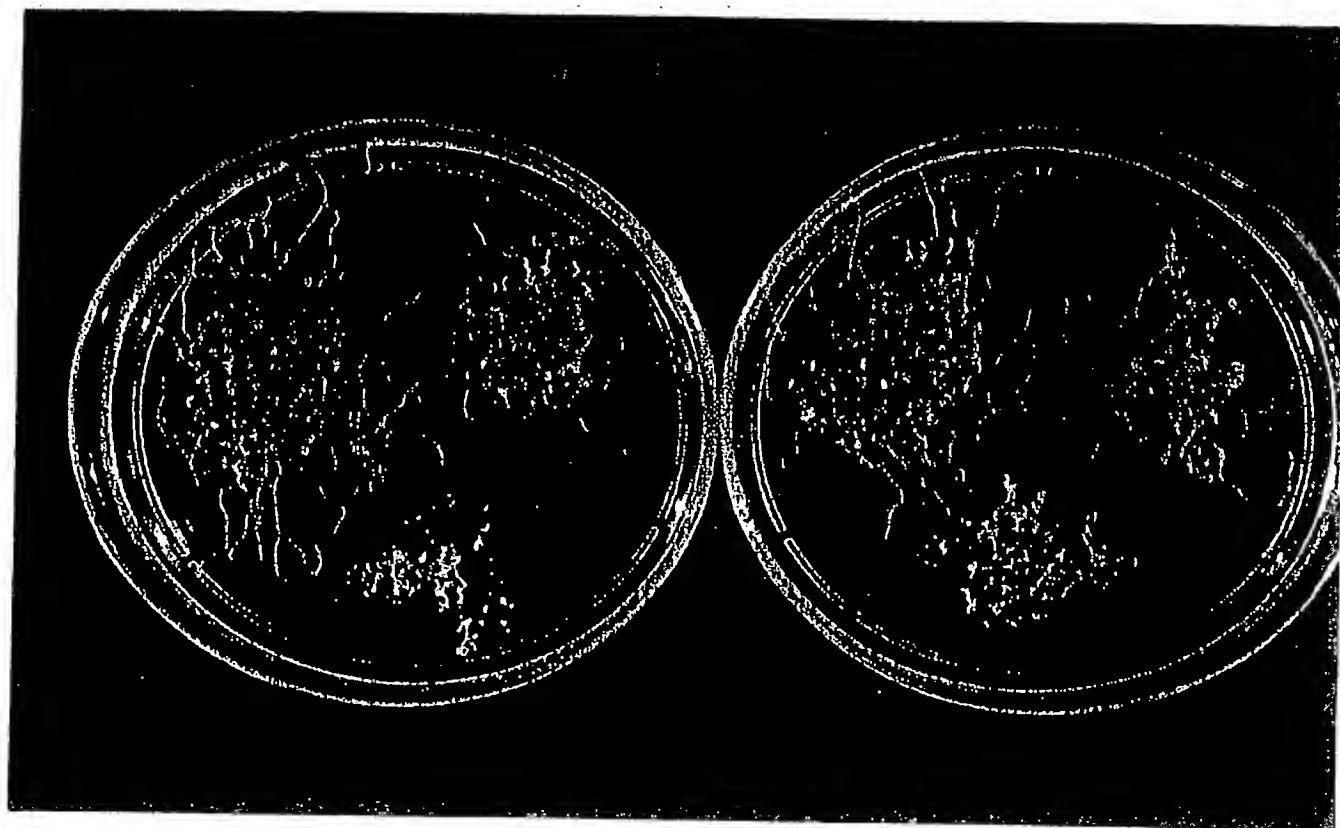


FIGURE 14

SEQUENCE LISTING

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<120> Genes involved in tolerance to environmental stress

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<140>

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<151> 1998-08-04

<160> 126

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              10              15              20

ttc ccc aat cag aac cta acg aaa aga aga acg cgt cca gcg ggt atc      150
Phe Pro Asn Gln Asn Leu Thr Lys Arg Arg Thr Arg Pro Ala Gly Ile
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acc tcc aac acg tca tta aag gaa gtg tcc cag ccc acg aaa tac agt      246
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Ser Asn Ser Pro Pro Val Ser Pro Ala Ile Phe Tyr Glu Arg Ala Thr
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Arg	His	Arg	Asn	Gly	Lys	Gln	Gly	Ser	Ser	Gly	Met	Leu	Phe	Asn	Gly					
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1909

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 35 40 45
 Phe Pro Tyr Glu Asp Thr Ser Asn Thr Ser Leu Lys Glu Val Ser Gln
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 Pro Thr Lys Tyr Ser Ser Asn Ser Pro Pro Val Ser Pro Ala Ile Phe
 65 70 75 80
 Tyr Glu Arg Ala Thr Ser Trp Cys Thr Gln Arg Val Val Ser Gly Arg
 85 90 95
 Ala Met Tyr Phe Leu Glu Tyr Tyr Cys Asp Met Phe Asp Tyr Val Ile
 100 105 110
 Ser Arg Arg Gln Arg Thr Lys Gln Val Leu Glu Tyr Leu Gln Gln Gln
 115 120 125
 Ser Gln Leu Pro Asn Ser Asp Gln Ile Lys Leu Asn Glu Glu Trp Ser
 130 135 140
 Ser Tyr Leu Gln Arg Glu His Gln Val Leu Ser Lys Arg Arg Leu Lys
 145 150 155 160
 Pro Lys Asn Arg Asp Phe Glu Met Ile Thr Gln Val Gly Gln Gly Gly
 165 170 175
 Tyr Gly His Val Tyr Leu Ala Arg Lys Lys Asp Thr Lys Glu Val Cys
 180 185 190
 Ala Leu Lys Ile Leu Asn Lys Lys Leu Gly Phe Lys Leu Asn Gly Thr
 195 200 205
 Cys His Val Leu Thr Glu Arg Gln Ser Leu Thr Thr Thr Arg Ser Glu
 210 215 220
 Thr Met Val Lys Leu Leu Ser Gly Thr Thr Pro Val Gly Ser Arg Gly
 225 230 235 240
 Met Ala Ile Glu Ser Glu Leu Gly Gly Asp Phe Arg Thr Glu Ser Ile
 245 250 255

Gly Arg Arg Cys Leu Lys Ser Gly His Ala Arg Phe Tyr Ile Ser Glu
 260 265 270
 Met Phe Cys Ala Val Asn Glu Lys His Leu Leu Ser Lys Thr Asp Ser
 275 280 285
 Thr Ile Ser Asn Glu Glu Asp Ser Ser Ile Asn Ile Arg Leu Glu Lys
 290 295 300
 Phe Lys Asp Leu Gly Tyr Pro Ala Leu Ser Glu Lys Ser Ile Glu Asp
 305 310 315 320
 Arg Arg Lys Leu Tyr Thr Cys Pro Asn Ser Met Val Gly Ser Pro Asp
 325 330 335
 Tyr Ile Ala Leu Glu Val Leu Arg Gly Lys Arg Tyr Glu Tyr Thr Val
 340 345 350
 Asp Tyr Trp Ser Leu Gly Cys Met Leu Phe Glu Ser Leu Val Gly Tyr
 355 360 365
 Thr Pro Phe Ser Gly Ser Ser Thr Asn Glu Thr Tyr Ala Ile Ser Arg
 370 375 380
 Ser Trp Lys Gln Thr Leu Asn Arg Ala Arg His Glu Asp Gly Arg Ala
 385 390 395 400
 Ala Phe Tyr Asn Arg Thr Trp Asp Leu Ile Thr Arg His Arg Ala Asp
 405 410 415
 Leu Ser Thr Arg Thr Arg Ser Phe Glu His Glu Val Lys Met Ser Tyr
 420 425 430
 Phe Ala Asp Ile Leu Phe Lys Ala Leu Arg Ser Ile Ile Pro Pro Phe
 435 440 445
 Thr Pro Gln Leu Asp Ser Glu Thr Asp Ala Gly Tyr Phe Asp Asp Phe
 450 455 460
 Trp Asn Glu Ala Asp Ile Ala Lys Tyr Ala Asp Val Phe Asn Ser Gln
 465 470 475 480
 Cys Cys Arg Thr Ala Leu Val Asp Asp Ser Ala Val Ser Ser Lys Leu
 485 490 495
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                               Met Asp Leu Glu Phe Gly Arg
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Phe Pro Ile Phe Ser Ile Leu Glu Asp Met Leu Glu Ala Pro Glu Glu
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caa acc gag aag act cgt aac aac cct tca aga gct tac atg cga gac 210
Gln Thr Glu Lys Thr Arg Asn Asn Pro Ser Arg Ala Tyr Met Arg Asp
          25          30          35

gca aag gca atg gct gct aca cca gct gac gtt atc gag cac ccg gat 258
Ala Lys Ala Met Ala Ala Thr Pro Ala Asp Val Ile Glu His Pro Asp
          40          45          50          55

gcg tac gtt ttc gcc gtg gac atg cct gga atc aaa gga gat gag att 306
Ala Tyr Val Phe Ala Val Asp Met Pro Gly Ile Lys Gly Asp Glu Ile
          60          65          70

cag gtc cag ata gag aac gag aac gtg ctt gtg gtg agt ggc aaa aga 354
Gln Val Gln Ile Glu Asn Glu Asn Val Leu Val Val Ser Gly Lys Arg
          75          80          85

cag agg gac aac aag gag aat gaa ggt gtg aag ttt gtg agg atg gag 402
Gln Arg Asp Asn Lys Glu Asn Glu Gly Val Lys Phe Val Arg Met Glu
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agg agg atg ggg aag ttt atg agg aag ttt cag tta cct gat aat gca 450
Arg Arg Met Gly Lys Phe Met Arg Lys Phe Gln Leu Pro Asp Asn Ala
          105          110          115

gat ttg gag aag atc tct gcg gct tgt aat gac ggt gtg ttg aaa gtg 498
Asp Leu Glu Lys Ile Ser Ala Ala Cys Asn Asp Gly Val Leu Lys Val
          120          125          130          135

act att ccg aaa ctt cct cct cct gag cca aag aaa cca aag act ata 546
Thr Ile Pro Lys Leu Pro Pro Pro Glu Pro Lys Lys Pro Lys Thr Ile
          140          145          150

caa gtt caa gtc gct tga gtttgtttgt gatccgtgtt tttgtgtttt 594
Gln Val Gln Val Ala
          155

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 35 40 45
 Asp Val Ile Glu His Pro Asp Ala Tyr Val Phe Ala Val Asp Met Pro
 50 55 60
 Gly Ile Lys Gly Asp Glu Ile Gln Val Gln Ile Glu Asn Glu Asn Val
 65 70 75 80
 Leu Val Val Ser Gly Lys Arg Gln Arg Asp Asn Lys Glu Asn Glu Gly
 85 90 95
 Val Lys Phe Val Arg Met Glu Arg Arg Met Gly Lys Phe Met Arg Lys
 100 105 110
 Phe Gln Leu Pro Asp Asn Ala Asp Leu Glu Lys Ile Ser Ala Ala Cys
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 ttccaatcat cc atg agt ccg gac aat aaa ctg ctt ccg aag cgg. atc atc 171
 Met Ser Pro Asp Asn Lys Leu Leu Pro Lys Arg Ile Ile
 1 5 10

ctt gta cgg cac ggt gaa tcg gaa ggg aat ctc gac acg gcg gcg tat 219
 Leu Val Arg His Gly Glu Ser Glu Gly Asn Leu Asp Thr Ala Ala Tyr
 15 20 25

aca acg acg ccg gat cat aag atc cag tta acg gat tcc ggt ttg ctt 267
 Thr Thr Thr Pro Asp His Lys Ile Gln Leu Thr Asp Ser Gly Leu Leu
 30 35 40 45

cag gcg cag gaa gcc gga gct cgt ctc cac gct ttg atc tct tct aat 315
 Gln Ala Gln Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn
 50 55 60

cct tct tca ccg gag tgg cgt gtg tac ttc tac gtt tcg ccg tac gat 363
 Pro Ser Ser Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp
 65 70 75

cgg act cga tct acg ctc cgg gag atc gga cgg tcg ttc tcg cgt cgc 411
 Arg Thr Arg Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg
 80 85 90

cgt gtg att ggt gtt cgc gaa gaa tgt cgg att agg gaa cag gat ttt 459
 Arg Val Ile Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe
 95 100 105

ggg aat ttt cag gtt aaa gag cga atg aga gca acg aaa aag gtc aga 507
 Gly Asn Phe Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg
 110 115 120 125

gag aga ttt ggc cgc ttt ttt tac cgg ttc ccg gag gga gaa tcc gcc 555
 Glu Arg Phe Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala
 130 135 140

gcc gat gtc ttc gat cgc gtc tcc agt ttt ctc gag tct cta tgg aga 603
 Ala Asp Val Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg
 145 150 155

gac att gac atg aac aga ctg cac atc aac ccg tct cat gag cta aac 651
 Asp Ile Asp Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn
 160 165 170

ttt gtg att gtc tca cat ggc tta aca tcg cgt gtg ttt ctg atg aaa 699
 Phe Val Ile Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys
 175 180 185

tgg ttt aag tgg tca gtg gaa cag ttc gag gga cta aac aat cca ggg 747
 Trp Phe Lys Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly
 190 195 200 205

aac agt gag atc aga gtg atg gaa tta gga caa ggc ggt gat tac agc 795
 Asn Ser Glu Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser
 210 215 220

ttg gcg att cat cac aca gag gaa gag tta gcc aca tgg gga ctg tca 843
 Leu Ala Ile His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser
 225 230 235

cca gag atg att gca gat caa aag tgg cgg gct aac gcg cat aaa ggc 891

Pro Glu Met Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly
 240 245 250

gaa tgg aaa gaa gat tgt aag tgg tat ttt ggt gat ttc ttc gac cat 939
 Glu Trp Lys Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His
 255 260 265

atg gca gat tcc gat aaa gag tgc gag act gag gcc act gaa gat aga 987
 Met Ala Asp Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg
 270 275 280 285

gaa gaa gaa gaa gaa gaa gag ggg aaa agg gta aat ctg cta acg agt 1035
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tca gaa tat agc aat gag cca gag tta tac aat gga caa tgc tgc tga 1083
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 305 310 315

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atttgatttt gataaaaact tgtaccaatt tactgattaa gctttctggt gtcttagttt 1203

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 35 40 45

Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn Pro Ser Ser
 50 55 60

Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp Arg Thr Arg
 65 70 75 80

Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg Arg Val Ile
 85 90 95

Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe Gly Asn Phe
 100 105 110

Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg Glu Arg Phe
 115 120 125

Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala Ala Asp Val
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 Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg Asp Ile Asp
 145 150 155 160
 Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn Phe Val Ile
 165 170 175
 Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys Trp Phe Lys
 180 185 190
 Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly Asn Ser Glu
 195 200 205
 Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser Leu Ala Ile
 210 215 220
 His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser Pro Glu Met
 225 230 235 240
 Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly Glu Trp Lys
 245 250 255
 Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His Met Ala Asp
 260 265 270
 Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg Glu Glu Glu
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 Val Ala Ile Ile Thr Gly Gly Ala Arg Gly Ile Gly Ala Ala Thr Ala
 15 20 25

aga ttg ttc aca gag aat ggc gcg tat gtg ata gtc gcg gat atc ctt	147
Arg Leu Phe Thr Glu Asn Gly Ala Tyr Val Ile Val Ala Asp Ile Leu	
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gat aat gaa ggc atc ctt gtg gcg gaa tcg atc ggt ggg tgt tac gtt	195
Asp Asn Glu Gly Ile Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val	
45 50 55	
cat tgt gac gta tcg aag gag gct gat gtt gag gcg gca gtg gag cta	243
His Cys Asp Val Ser Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu	
60 65 70 75	
gca atg aga cgt aaa ggt aga cta gat gtg atg ttc aac aat gcc ggg	291
Ala Met Arg Arg Lys Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly	
80 85 90	
atg tcg ctt aac gaa ggt agt atc atg ggg atg gac gtg gac atg gtt	339
Met Ser Leu Asn Glu Gly Ser Ile Met Gly Met Asp Val Asp Met Val	
95 100 105	
aac aaa ctt gtc tcg gtt aat gtc aat ggt gtt ttg cat ggt atc aaa	387
Asn Lys Leu Val Ser Val Asn Val Asn Gly Val Leu His Gly Ile Lys	
110 115 120	
cat gcc gct aag gcc atg atc aaa ggg gga cga gga ggc tcg ata ata	435
His Ala Ala Lys Ala Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile	
125 130 135	
tgc aca tcg agc tca tca ggg cta atg gga gga ctt gga gga cat gcg	483
Cys Thr Ser Ser Ser Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala	
140 145 150 155	
tat acg ctc tcc aaa gga ggc atc aac ggg gtg gtg agg aca acg gag	531
Tyr Thr Leu Ser Lys Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu	
160 165 170	
tgc gag ctt ggg tct cac ggc atc cgt gtg aat agc atc tct cct cat	579
Cys Glu Leu Gly Ser His Gly Ile Arg Val Asn Ser Ile Ser Pro His	
175 180 185	
gga gtt ccc act gac atc ttg gtt aat gcg tac cgt aag ttc ctt aac	627
Gly Val Pro Thr Asp Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn	
190 195 200	
aat gac aaa ctc aac gtc gct gag gtc acc gac att att gct gag aaa	675
Asn Asp Lys Leu Asn Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys	
205 210 215	
ggg agt ttg ctg acc gga aga gcc ggt act gtg gag gac gta gct caa	723
Gly Ser Leu Leu Thr Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln	
220 225 230 235	
gca gct ttg ttt ctt gca agc caa gaa tcg tcg ggg ttc att acc gga	771
Ala Ala Leu Phe Leu Ala Ser Gln Glu Ser Ser Gly Phe Ile Thr Gly	
240 245 250	
cat aac ttg gtt gtt gat ggt ggt tac aca tct gcc act agt act atg	819

His Asn Leu Val Val Asp Gly Gly Tyr Thr Ser Ala Thr Ser Thr Met
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863

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 35 40 45
 Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val His Cys Asp Val Ser
 50 55 60
 Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu Ala Met Arg Arg Lys
 65 70 75 80
 Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly Met Ser Leu Asn Glu
 85 90 95
 Gly Ser Ile Met Gly Met Asp Val Asp Met Val Asn Lys Leu Val Ser
 100 105 110
 Val Asn Val Asn Gly Val Leu His Gly Ile Lys His Ala Ala Lys Ala
 115 120 125
 Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile Cys Thr Ser Ser Ser
 130 135 140
 Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala Tyr Thr Leu Ser Lys
 145 150 155 160
 Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu Cys Glu Leu Gly Ser
 165 170 175
 His Gly Ile Arg Val Asn Ser Ile Ser Pro His Gly Val Pro Thr Asp
 180 185 190
 Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn Asn Asp Lys Leu Asn
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 Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys Gly Ser Leu Leu Thr
 210 215 220
 Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln Ala Ala Leu Phe Leu

225		230		235		240									
Ala	Ser	Gln	Glu	Ser	Ser	Gly	Phe	Ile	Thr	Gly	His	Asn	Leu	Val	Val
				245					250					255	
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 Arg G
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 ly Pro Val Leu
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 Arg Ile Pro Glu Arg Val Val His Ala Arg Gly Ile Ser Ala Lys Gly
 60 65 70
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 Phe Phe Glu Val Thr His Asp Ile Ser Asn Leu Thr Cys Ala Asp Phe
 75 80 85
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 125 130

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gttatgatca g gga aac ttt gat ctt gtt ggg aac aac act ccg gtg ttc 1616
 Gly Asn Phe Asp Leu Val Gly Asn Asn Thr Pro Val Phe
 135 140

ttc atc cgt gat ggg att cag ttc ccg gat gtt gtc cac gcg ttg aaa 1664
 Phe Ile Arg Asp Gly Ile Gln Phe Pro Asp Val Val His Ala Leu Lys
 145 150 155

cct aac cga aaa aca aac atc caa gag tac tgg agg att ctg gac tac 1712
 Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr
 160 165 170 175

atg tcc cac ttg cct gag agt ttg ctc aca tgg tgc tgg atg ttt gat 1760
 Met Ser His Leu Pro Glu Ser Leu Leu Thr Trp Cys Trp Met Phe Asp
 180 185 190

gat gtt ggt att cca caa gat tac agg cat atg gag ggt ttc ggt gtc 1808
 Asp Val Gly Ile Pro Gln Asp Tyr Arg His Met Glu Gly Phe Gly Val
 195 200 205

cac acc tac act ctt att gcc aaa tct gga aaa gtt ctc ttt gtg aag 1856
 His Thr Tyr Thr Leu Ile Ala Lys Ser Gly Lys Val Leu Phe Val Lys
 210 215 220

ttc cac tgg aaa cca act tgt ggg atc aag aat ctg act gat gaa gag 1904
 Phe His Trp Lys Pro Thr Cys Gly Ile Lys Asn Leu Thr Asp Glu Glu
 225 230 235

gcc aag gtt gtt gga gga gcc aat cac agc cac gcc act aag gat ctc 1952
 Ala Lys Val Val Gly Gly Ala Asn His Ser His Ala Thr Lys Asp Leu
 240 245 250 255

cac gat gcc att gca tct ggc aac tac ccc gag tgg aaa ctt ttc atc 2000
 His Asp Ala Ile Ala Ser Gly Asn Tyr Pro Glu Trp Lys Leu Phe Ile
 260 265 270

cag acc atg gat cct gca gat gag gat aag ttt gac ttt gac cca ctt 2048
 Gln Thr Met Asp Pro Ala Asp Glu Asp Lys Phe Asp Phe Asp Pro Leu
 275 280 285

gat gtg acc aag atc tgg cct gag gat att ttg cct ctg caa ccg gtt 2096
 Asp Val Thr Lys Ile Trp Pro Glu Asp Ile Leu Pro Leu Gln Pro Val
 290 295 300

ggt cgc ttg gtt ctg aac agg acc att gac aac ttc ttc aat gaa act 2144
 Gly Arg Leu Val Leu Asn Arg Thr Ile Asp Asn Phe Phe Asn Glu Thr
 305 310 315

gag cag ctt gcg ttc aac ccg ggt ctt gtg gtt cct gga atc tac tac 2192
 Glu Gln Leu Ala Phe Asn Pro Gly Leu Val Val Pro Gly Ile Tyr Tyr

320	325	330	335	
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Ser Asp Asp Lys Leu Leu Gln Cys Arg Ile Phe Ala Tyr Gly Asp Thr	340	345	350	
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Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Val Asn Ala	355	360	365	
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Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe	370	375	380	
atg cac aga gat gag gag gtacgtctta gtacaccact tgagctacca				2384
Met His Arg Asp Glu Glu	385			
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			Ile	390
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Pro Thr Pro Thr Asn Ser Tyr Thr Gly Ile Arg Thr Lys	410	415		
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Phe Lys Gln Ala Gly Asp Arg Tyr Arg Ser Trp Ala Pro Asp Arg Gln	430	435	440	
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Asp Arg Phe Val Lys Arg Trp Val Glu Ile Leu Ser Glu Pro Arg Leu	445	450	455	
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Thr His Glu Ile Arg Gly Ile Trp Thr Ser Tyr Trp Leu Lys	460	465	470	
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		Ala Asp Arg Ser Leu Gly Gln	480	
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Lys Leu Ala Ser Arg Leu Asn Val Arg Pro Ser Ile	485	490		

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Gln Ala Glu Ile Asn Gln Leu Leu Ser Leu Ile Ile Asn Thr Phe Tyr
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Asp Val Leu Asp Ala Ile Thr Lys His Leu Asp Ile Gly Ser Ser Tyr	
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Ser Gly Lys Arg Pro Leu Phe Gly Pro Asp Leu Pro Lys Thr Glu Glu	
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Ile Ser Asp Val Leu Asp Thr Phe Lys Val Ile Ser Glu Leu Pro Ser	
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Asp Cys Phe Gly Ala Tyr Ile Ile Ser Met Ala Thr Ser Pro Ser Asp	
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Val Leu Ala Val Glu Leu Leu Gln Arg Glu Cys His Val Lys Asn Pro	
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Leu Arg Val Val Pro Leu Phe Glu Lys Leu Ala Asp Leu Glu Ala Ala	
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Glu Leu Val Lys Val Ala Lys Lys Tyr Gly Val Lys Leu Thr Met Phe	
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Cys Phe Arg Thr Leu Gln Arg Phe Thr Ala Ala Thr Leu Glu His Gly	
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Gly Gly Ile Glu Ser Leu Arg Ala Ile Pro Trp Ile Phe Ala Trp Thr	
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Gln Thr Arg Phe His Leu Pro Val Trp Leu Gly Phe Gly Ala Ala Phe	
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 Asp Ser Tyr Ile Thr Thr Leu Asn Val Cys Gln Ala Tyr Thr Leu Lys
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Arg Leu Val Ser Asp Leu Gly Lys Ser Pro Glu Glu Ile Phe Asp Ala		
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Ser Val Arg Arg Ser Leu Leu Gln Lys His Gly Arg Ile Arg Asp Cys		
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Leu Ala Gln Leu Tyr Ala Lys Asp Ile Thr Pro Asp Asp Lys Gln Glu		
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Arg Asp Gly Asn Pro Arg Val Thr Pro Glu Val Thr Arg Asp Val Cys		
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Glu	Gly	Arg	Gln	Glu	Trp	Leu	Leu	Ala	Glu	Leu	Ser	Gly	Lys	Arg	Pro
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Gly Ser Ala Val Val Ala Tyr Val Cys Asp Lys Val Ile Ser Asp Asp
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Lys Leu Phe Gly Gly Thr Thr Pro Gly Thr Ile Thr Asn Lys Glu Trp
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ggt gct gcg act gaa gag aga tta caa gca tgg cca aga gtt gct ggt 196
Gly Ala Ala Thr Glu Glu Arg Leu Gln Ala Trp Pro Arg Val Ala Gly
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200 205 210

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Pro Glu Phe Arg Arg Leu Val Glu Leu Tyr Ala
215 220

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 Gly Val Lys Ala Lys His Pro Lys Ile Thr Tyr Ala Asp Leu Tyr Gln
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Glu	Phe	His	Lys	Ser	His	Gly	Gly	Glu	Ala	Ser	Ile	Met	Val	Thr	Lys						
		125					130					135									
gtg	gat	gaa	ccg	tcg	aaa	tat	gga	gtg	gtt	gtt	atg	gaa	gaa	agc	act	483					
Val	Asp	Glu	Pro	Ser	Lys	Tyr	Gly	Val	Val	Val	Met	Glu	Glu	Ser	Thr						
	140					145					150										
gga	aga	gtg	gag	aag	ttt	gtg	gaa	aag	cca	aaa	ctg	tat	gta	ggg	aac	531					
Gly	Arg	Val	Glu	Lys	Phe	Val	Glu	Lys	Pro	Lys	Leu	Tyr	Val	Gly	Asn						
155					160					165					170						
aag	atc	aac	gct	ggg	att	tat	ctt	ctg	aac	cca	tct	gtt	ctt	gat	aag	579					
Lys	Ile	Asn	Ala	Gly	Ile	Tyr	Leu	Leu	Asn	Pro	Ser	Val	Leu	Asp	Lys						
				175					180					185							
att	gag	cta	aga	ccg	act	tca	atc	gaa	aaa	gag	act	ttc	cct	aag	att	627					
Ile	Glu	Leu	Arg	Pro	Thr	Ser	Ile	Glu	Lys	Glu	Thr	Phe	Pro	Lys	Ile						
			190					195					200								
gca	gca	gcg	caa	ggg	ctc	tat	gct	atg	gtg	cta	cca	ggg	ttt	tgg	atg	675					
Ala	Ala	Ala	Gln	Gly	Leu	Tyr	Ala	Met	Val	Leu	Pro	Gly	Phe	Trp	Met						
		205					210					215									
gac	att	ggg	caa	ccc	cgt	gac	tac	ata	acg	ggg	ttg	aga	ctc	tac	tta	723					
Asp	Ile	Gly	Gln	Pro	Arg	Asp	Tyr	Ile	Thr	Gly	Leu	Arg	Leu	Tyr	Leu						
	220					225					230										
gac	tcc	ctt	agg	aag	aaa	tct	cct	gcc	aaa	tta	acc	agt	ggg	cca	cac	771					
Asp	Ser	Leu	Arg	Lys	Lys	Ser	Pro	Ala	Lys	Leu	Thr	Ser	Gly	Pro	His						
235					240					245					250						
ata	gtt	ggg	aat	gtt	ctt	gtt	gac	gaa	acc	gct	aca	att	ggg	gaa	gga	819					
Ile	Val	Gly	Asn	Val	Leu	Val	Asp	Glu	Thr	Ala	Thr	Ile	Gly	Glu	Gly						
				255				260						265							
tgt	ttg	att	gga	cca	gac	gtt	gcc	att	ggg	cca	ggc	tgc	att	gtt	gag	867					
Cys	Leu	Ile	Gly	Pro	Asp	Val	Ala	Ile	Gly	Pro	Gly	Cys	Ile	Val	Glu						
			270					275					280								
tca	gga	gtc	aga	ctc	tcc	cga	tgc	acg	gtc	atg	cgt	gga	gtc	cgc	atc	915					
Ser	Gly	Val	Arg	Leu	Ser	Arg	Cys	Thr	Val	Met	Arg	Gly	Val	Arg	Ile						
		285					290					295									
aag	aag	cat	gcg	tgt	atc	tcg	agc	agt	atc	atc	ggg	tgg	cac	tca	acg	963					
Lys	Lys	His	Ala	Cys	Ile	Ser	Ser	Ser	Ile	Ile	Gly	Trp	His	Ser	Thr						
	300					305					310										
gtt	ggg	caa	tgg	gcc	agg	atc	gag	aac	atg	acg	atc	ctc	ggg	gag	gat	1011					
Val	Gly	Gln	Trp	Ala	Arg	Ile	Glu	Asn	Met	Thr	Ile	Leu	Gly	Glu	Asp						
315					320					325					330						

gtt cat gtg agc gat gag atc tat agc aat gga gga gtt gtt ttg cca 1059
 Val His Val Ser Asp Glu Ile Tyr Ser Asn Gly Gly Val Val Leu Pro
 335 340 345

cac aag gag atc aaa tca aac atc ttg aag cca gag ata gtg atg tga 1107
 His Lys Glu Ile Lys Ser Asn Ile Leu Lys Pro Glu Ile Val Met
 350 355 360

aa 1109

<210> 24

<211> 361

<212> PRT

<213> Arabidopsis thaliana

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Met Ile Leu His Gln Ile Glu Ala Leu Lys Ala Val Gly Val Asp Glu
 35 40 45

Val Val Leu Ala Ile Asn Tyr Gln Pro Glu Val Met Leu Asn Phe Leu
 50 55 60

Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys Ile Thr Cys Ser Gln Glu
 65 70 75 80

Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu Ala Leu Ala Arg Asp Lys
 85 90 95

Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe Val Leu Asn Ser Asp Val
 100 105 110

Ile Ser Glu Tyr Pro Leu Lys Glu Met Leu Glu Phe His Lys Ser His
 115 120 125

Gly Gly Glu Ala Ser Ile Met Val Thr Lys Val Asp Glu Pro Ser Lys
 130 135 140

Tyr Gly Val Val Val Met Glu Glu Ser Thr Gly Arg Val Glu Lys Phe
 145 150 155 160

Val Glu Lys Pro Lys Leu Tyr Val Gly Asn Lys Ile Asn Ala Gly Ile
 165 170 175

Tyr Leu Leu Asn Pro Ser Val Leu Asp Lys Ile Glu Leu Arg Pro Thr
 180 185 190

Ser Ile Glu Lys Glu Thr Phe Pro Lys Ile Ala Ala Ala Gln Gly Leu
 195 200 205

Tyr Ala Met Val Leu Pro Gly Phe Trp Met Asp Ile Gly Gln Pro Arg
 210 215 220
 Asp Tyr Ile Thr Gly Leu Arg Leu Tyr Leu Asp Ser Leu Arg Lys Lys
 225 230 235 240
 Ser Pro Ala Lys Leu Thr Ser Gly Pro His Ile Val Gly Asn Val Leu
 245 250 255
 Val Asp Glu Thr Ala Thr Ile Gly Glu Gly Cys Leu Ile Gly Pro Asp
 260 265 270
 Val Ala Ile Gly Pro Gly Cys Ile Val Glu Ser Gly Val Arg Leu Ser
 275 280 285
 Arg Cys Thr Val Met Arg Gly Val Arg Ile Lys Lys His Ala Cys Ile
 290 295 300
 Ser Ser Ser Ile Ile Gly Trp His Ser Thr Val Gly Gln Trp Ala Arg
 305 310 315 320
 Ile Glu Asn Met Thr Ile Leu Gly Glu Asp Val His Val Ser Asp Glu
 325 330 335
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 cct tat cga acc aac tct tct ttc ggc tca aag tca tcg ctt ctc ttt 98
 Pro Tyr Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe
 15 20 25 30
 cgg tct cca tcc tcc tcc tcc tca gtc tct atg acg aca acg cgt gga 146
 Arg Ser Pro Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly
 35 40 45
 aac gtg gct gtg gcg gct gct gct aca tcc act gag gcg cta aga aaa 194
 Asn Val Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys
 50 55 60

gga ata gcg gag ttc tac aat gaa act tcg ggt ttg tgg gaa gag att	242
Gly Ile Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile	
65 70 75	
tgg gga gat cat atg cat cat ggc ttt tat gac cct gat tct tct gtt	290
Trp Gly Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val	
80 85 90	
caa ctt tct gat tct ggt cac aag gaa gct cag atc cgt atg att gaa	338
Gln Leu Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu	
95 100 105 110	
gag tct ctc cgt ttc gcc ggt gtt act gat gaa gag gag gag aaa aag	386
Glu Ser Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys	
115 120 125	
ata aag aaa gta gtg gat gtt ggg tgt ggg att gga gga agc tca aga	434
Ile Lys Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg	
130 135 140	
tat ctt gcc tct aaa ttt gga gct gaa tgc att ggc att act ctc agc	482
Tyr Leu Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser	
145 150 155	
cct gtt cag gcc aag aga gcc aat gat ctc gcg gct gct caa tca ctc	530
Pro Val Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu	
160 165 170	
tct cat aag gct tcc ttc caa gtt gcg gat gcg ttg gat cag cca ttc	578
Ser His Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe	
175 180 185 190	
gaa gat gga aaa ttc gat cta gtg tgg tcg atg gag agt ggt gag cat	626
Glu Asp Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His	
195 200 205	
atg cct gac aag gcc aag ttt gta aaa gag ttg gta cgt gtg gcg gct	674
Met Pro Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala	
210 215 220	
cca gga ggt agg ata ata ata gtg aca tgg tgc cat aga aat cta tct	722
Pro Gly Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser	
225 230 235	
gcg ggg gag gaa gct ttg cag ccg tgg gag caa aac atc ttg gac aaa	770
Ala Gly Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys	
240 245 250	
atc tgt aag acg ttc tat ctc ccg gct tgg tgc tcc acc gat gat tat	818
Ile Cys Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr	
255 260 265 270	
gtc aac ttg ctt caa tcc cat tct ctc cag gat att aag tgt gcg gat	866
Val Asn Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp	
275 280 285	

tgg tca gag aac gta gct cct ttc tgg cct gcg gtt ata cgg act gca 914
 Trp Ser Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala
 290 295 300
 tta aca tgg aag ggc ctt gtg tct ctg ctt cgt agt ggt atg aaa agt 962
 Leu Thr Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser
 305 310 315
 att aaa gga gca ttg aca atg cca ttg atg att gaa ggt tac aag aaa 1010
 Ile Lys Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys
 320 325 330
 ggt gtc att aag ttt ggt atc atc act tgc cag aag cca ctc taa 1055
 Gly Val Ile Lys Phe Gly Ile Ile Thr Cys Gln Lys Pro Leu
 335 340 345
 gtctaaagct atacta 1071

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 <212> PRT
 <213> Arabidopsis thaliana

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 Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly Asn Val
 35 40 45
 Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys Gly Ile
 50 55 60
 Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile Trp Gly
 65 70 75 80
 Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val Gln Leu
 85 90 95
 Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu Glu Ser
 100 105 110
 Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys Ile Lys
 115 120 125
 Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Tyr Leu
 130 135 140
 Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser Pro Val
 145 150 155 160
 Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu Ser His
 165 170 175

Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe Glu Asp
 180 185 190
 Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His Met Pro
 195 200 205
 Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala Pro Gly
 210 215 220
 Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser Ala Gly
 225 230 235 240
 Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys Ile Cys
 245 250 255
 Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr Val Asn
 260 265 270
 Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp Trp Ser
 275 280 285
 Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala Leu Thr
 290 295 300
 Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser Ile Lys
 305 310 315 320
 Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys Gly Val
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 Ile Lys Phe Gly Ile Ile Thr Cys Gln Lys Pro Leu
 340 345

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 ctc gag atc gac gat gac cag aaa cta cgt gcg ttt tac gac aag aga 95
 Leu Glu Ile Asp Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg
 20 25 30
 atc tct caa gaa gtc agt gga gat gct ttg ggc gag gag ttc aaa gga 143
 Ile Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly
 35 40 45

tac gtt ttc aag atc aag ggt ggt tgc gat aag caa ggt ttc cca atg	191
Tyr Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met	
50 55 60	
aag cag gga gtt ttg act cca ggc cgt gtt cgc ctt ttg ctt cac cga	239
Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg	
65 70 75	
gga act cct tgc ttc aga gga cat gga agg aga act ggt gag agg aga	287
Gly Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg	
80 85 90 95	
aga aag tct gtt cgt ggt tgc att gtg agc cct gat ctc tct gtt ctg	335
Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu	
100 105 110	
aac ctt gtc att gtg aag aag ggt gag aac gat ctt cct ggg ctt acc	383
Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr	
115 120 125	
gat cat gag agc aag atg aga gga cca aag aga gcc tcc aag atc cgt	431
Asp His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg	
130 135 140	
aaa ctg ttt aac ctc aag aag gaa gat gat gtc agg acc tat gtc aac	479
Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn	
145 150 155	
act tac cgc cgc aag ttc aca aac aag aag ggc aag gaa gtt agc aaa	527
Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys	
160 165 170 175	
gcc cct aag atc cag agg ctt gtg acc cca ttg act ctt cag agg aag	575
Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys	
180 185 190	
aga gct aga att gct gac aag aag aag aaa att gct aag gct aat tct	623
Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser	
195 200 205	
gat gct gct gat tac cag aag ctt ctc gcc tcg agg ttg aag gaa cag	671
Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln	
210 215 220	
cgt gac agg agg agt gag agt ttg gca aaa gag agg tcg aga ctc tct	719
Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser	
225 230 235	
tct gct gct gcc aag ccc tct gtc aca gct taa aaaagcttga gattca	768
Ser Ala Ala Ala Lys Pro Ser Val Thr Ala	
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<212> PRT	

<213> Arabidopsis thaliana

<400> 28

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 20 25 30
 Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly Tyr
 35 40 45
 Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys
 50 55 60
 Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly
 65 70 75 80
 Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg
 85 90 95
 Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn
 100 105 110
 Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp
 115 120 125
 His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys
 130 135 140
 Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr
 145 150 155 160
 Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala
 165 170 175
 Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg
 180 185 190
 Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp
 195 200 205
 Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg
 210 215 220
 Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser Ser
 225 230 235 240
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<210> 29

<211> 1201

<212> DNA

<213> Arabidopsis thaliana

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 ctcttctctt ttctctgtca ctaattttca g act gag aaa gct ttt ctt aag 167
 Thr Glu Lys Ala Phe Leu Lys
 5 10

cag cct aag gtc ttc ctt ag gtaattttgc gattcgattt ctctctgttc 217
 Gln Pro Lys Val Phe Leu Se
 15

tctattgttt cattgtattt aagttccaag ttgtttatat tgttcattgt ttctgattta 277

tcaag c tcg aag aaa tct gga aag gga aag aga cct gga aaa ggt gga 325
 r Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly
 20 25 30

aac cgt ttc tgg aag aac att ggt ttg ggc ttc aag act cct cgt gaa 373
 Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu
 35 40 45

gcc att gat g gtatgtttta gcttttaact cgttataata gataaggaac 423
 Ala Ile Asp G
 50

tcttggattg tgttgttcat atagtcgata gatttcaaata gctattttgt cttgtagaat 483

cttaagcttt ggttttagtga gttctgattc ttcagcttta tctggatcta cattactgtt 543

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 Gly Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg
 35 40 45
 Glu Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly
 50 55 60
 Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala
 65 70 75 8
 Lys Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val
 85 90 95
 Lys Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His
 100 105 110
 Val Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly
 115 120 125
 Gln Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val
 130 135 140
 Ile Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys Lys Ala Phe Thr Gly
 145 150 155 16
 Met

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 <211> 1790
 <212> DNA
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 <222> (23)..(1780)

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 Leu Ile Glu Glu Gly Leu Ile Leu Gln Glu Val Lys Leu Tyr Ala Glu
 15 20 25
 gat ggt tca gtg gac ttt aat gga aac cca cca ttg aag gag aaa aca 148
 Asp Gly Ser Val Asp Phe Asn Gly Asn Pro Pro Leu Lys Glu Lys Thr
 30 35 40
 gga aac tgg aaa gct tgt cct ttt att ctt ggt aat gaa tgt tgt gag 196
 Gly Asn Trp Lys Ala Cys Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu
 45 50 55

agg cta gct tac tat ggt att gct ggg aat tta atc act tac ctc acc	244
Arg Leu Ala Tyr Tyr Gly Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr	
60 65 70	
act aag ctt cac caa gga aat gtt tct gct gct aca aac gtt acc aca	292
Thr Lys Leu His Gln Gly Asn Val Ser Ala Ala Thr Asn Val Thr Thr	
75 80 85 90	
tgg caa ggg act tgt tat ctc act cct ctc att gga gct gtt ctg gct	340
Trp Gln Gly Thr Cys Tyr Leu Thr Pro Leu Ile Gly Ala Val Leu Ala	
95 100 105	
gat gct tac tgg gga cgt tac tgg acc atc gct tgt ttc tcc ggg att	388
Asp Ala Tyr Trp Gly Arg Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile	
110 115 120	
tat ttc atc ggg atg tct gcg tta act ctt tca gct tca gtt ccg gca	436
Tyr Phe Ile Gly Met Ser Ala Leu Thr Leu Ser Ala Ser Val Pro Ala	
125 130 135	
ttg aag cca gcg gaa tgt att ggt gac ttt tgt cca tct gca acg cca	484
Leu Lys Pro Ala Glu Cys Ile Gly Asp Phe Cys Pro Ser Ala Thr Pro	
140 145 150	
gct cag tat gcg atg ttc ttt ggt ggg ctt tac ctg atc gct ctt gga	532
Ala Gln Tyr Ala Met Phe Phe Gly Gly Leu Tyr Leu Ile Ala Leu Gly	
155 160 165 170	
act gga ggt atc aaa ccg tgt gtc tca tcc ttc ggt gcc gat cag ttt	580
Thr Gly Gly Ile Lys Pro Cys Val Ser Ser Phe Gly Ala Asp Gln Phe	
175 180 185	
gat gac acg gac tct ccg gaa cga gtt aga aaa gct tcg ttc ttt aac	628
Asp Asp Thr Asp Ser Arg Glu Arg Val Arg Lys Ala Ser Phe Phe Asn	
190 195 200	
tgg ttt tac ttc tcc atc aat att gga gca ctt gtg tca tct agt ctt	676
Trp Phe Tyr Phe Ser Ile Asn Ile Gly Ala Leu Val Ser Ser Ser Leu	
205 210 215	
cta gtt tgg att caa gag aat ccg ggg tgg ggt tta ggg ttt ggg ata	724
Leu Val Trp Ile Gln Glu Asn Arg Gly Trp Gly Leu Gly Phe Gly Ile	
220 225 230	
cca aca gtg ttc atg gga cta gcc att gca agt ttc ttc ttt ggc aca	772
Pro Thr Val Phe Met Gly Leu Ala Ile Ala Ser Phe Phe Phe Gly Thr	
235 240 245 250	
cct ctt tat agg ttt cag aaa cct gga gga agc cct ata act ccg att	820
Pro Leu Tyr Arg Phe Gln Lys Pro Gly Gly Ser Pro Ile Thr Arg Ile	
255 260 265	
tcc caa gtc gtg gtt gct tcg ttc ccg aaa tcg tct gtc aaa gtc cct	868
Ser Gln Val Val Val Ala Ser Phe Arg Lys Ser Ser Val Lys Val Pro	
270 275 280	
gaa gac gcc aca ctt ctg tat gaa act caa gac aag aac tct gct att	916

Glu Asp Ala Thr Leu Leu Tyr Glu Thr Gln Asp Lys Asn Ser Ala Ile	
285	290 295
gct gga agt aga aaa atc gag cat acc gat gat tgc cag tat ctt gac	964
Ala Gly Ser Arg Lys Ile Glu His Thr Asp Asp Cys Gln Tyr Leu Asp	
300	305 310
aaa gcc gct gtt atc tca gaa gaa gaa tcg aaa tcc gga gat tat tcc	1012
Lys Ala Ala Val Ile Ser Glu Glu Glu Ser Lys Ser Gly Asp Tyr Ser	
315	320 325 330
aac tcg tgg aga cta tgc acg gtt acg caa gtc gaa gaa ctc aag att	1060
Asn Ser Trp Arg Leu Cys Thr Val Thr Gln Val Glu Glu Leu Lys Ile	
	335 340 345
ctg atc cga atg ttc cca atc tgg gct tct ggt atc att ttc tca gct	1108
Leu Ile Arg Met Phe Pro Ile Trp Ala Ser Gly Ile Ile Phe Ser Ala	
	350 355 360
gta tac gca caa atg tcc aca atg ttt gtt caa caa ggc cga gcc atg	1156
Val Tyr Ala Gln Met Ser Thr Met Phe Val Gln Gln Gly Arg Ala Met	
	365 370 375
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Asn Cys Lys Ile Gly Ser Phe Gln Leu Pro Pro Ala Ala Leu Gly Thr	
	380 385 390
ttc gac aca gca agc gtc atc atc tgg gtg ccg ctc tac gac cgg ttc	1252
Phe Asp Thr Ala Ser Val Ile Ile Trp Val Pro Leu Tyr Asp Arg Phe	
	395 400 405 410
atc gtt ccc tta gca aga aag ttc aca gga gta gac aaa gga ttc act	1300
Ile Val Pro Leu Ala Arg Lys Phe Thr Gly Val Asp Lys Gly Phe Thr	
	415 420 425
gag ata caa aga atg gga att ggt ctg ttt gtc tct gtt ctc tgt atg	1348
Glu Ile Gln Arg Met Gly Ile Gly Leu Phe Val Ser Val Leu Cys Met	
	430 435 440
gca gct gca gct atc gtc gaa atc atc cgt ctc cat atg gcc aac gat	1396
Ala Ala Ala Ala Ile Val Glu Ile Ile Arg Leu His Met Ala Asn Asp	
	445 450 455
ctt gga tta gtc gag tca gga gcc cca gtt ccc ata tcc gtc ttg tgg	1444
Leu Gly Leu Val Glu Ser Gly Ala Pro Val Pro Ile Ser Val Leu Trp	
	460 465 470
cag att cca cag tac ttc att ctc ggt gca gcc gaa gta ttc tac ttc	1492
Gln Ile Pro Gln Tyr Phe Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe	
	475 480 485 490
atc ggt cag ctc gag ttc ttc tac gac caa tct cca gat gca atg aga	1540
Ile Gly Gln Leu Glu Phe Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg	
	495 500 505
agc ttg tgc agt gcc tta gct ctt ttg acc aat gca ctt ggt aac tac	1588
Ser Leu Cys Ser Ala Leu Ala Leu Leu Thr Asn Ala Leu Gly Asn Tyr	

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Leu	Ser	Ser	Leu	Ile	Leu	Thr	Leu	Val	Thr	Tyr	Phe	Thr	Thr	Arg	Asn	
		525					530					535				
ggg	caa	gaa	ggg	tgg	att	tcg	gat	aat	ctc	aat	tca	ggg	cat	ctc	gat	1684
Gly	Gln	Glu	Gly	Trp	Ile	Ser	Asp	Asn	Leu	Asn	Ser	Gly	His	Leu	Asp	
	540					545					550					
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Tyr	Phe	Phe	Trp	Leu	Leu	Ala	Gly	Leu	Ser	Leu	Val	Asn	Met	Ala	Val	
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tac	ttc	ttc	tct	gct	gct	agg	tat	aag	caa	aag	aaa	gct	tcg	tcg	tag	1780
Tyr	Phe	Phe	Ser	Ala	Ala	Arg	Tyr	Lys	Gln	Lys	Lys	Ala	Ser	Ser		
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Asn	Val	Ser	Ala	Ala	Thr	Asn	Val	Thr	Thr	Trp	Gln	Gly	Thr	Cys	Tyr
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Leu	Thr	Pro	Leu	Ile	Gly	Ala	Val	Leu	Ala	Asp	Ala	Tyr	Trp	Gly	Arg
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 Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Arg
 180 185 190
 Glu Arg Val Arg Lys Ala Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile
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 Asn Ile Gly Ala Leu Val Ser Ser Ser Leu Leu Val Trp Ile Gln Glu
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 Asn Arg Gly Trp Gly Leu Gly Phe Gly Ile Pro Thr Val Phe Met Gly
 225 230 235 240
 Leu Ala Ile Ala Ser Phe Phe Phe Gly Thr Pro Leu Tyr Arg Phe Gln
 245 250 255
 Lys Pro Gly Gly Ser Pro Ile Thr Arg Ile Ser Gln Val Val Val Ala
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 Ser Phe Arg Lys Ser Ser Val Lys Val Pro Glu Asp Ala Thr Leu Leu
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 Tyr Glu Thr Gln Asp Lys Asn Ser Ala Ile Ala Gly Ser Arg Lys Ile
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 Glu His Thr Asp Asp Cys Gln Tyr Leu Asp Lys Ala Ala Val Ile Ser
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 Thr Val Thr Gln Val Glu Glu Leu Lys Ile Leu Ile Arg Met Phe Pro
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 Ile Trp Ala Ser Gly Ile Ile Phe Ser Ala Val Tyr Ala Gln Met Ser
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 Thr Met Phe Val Gln Gln Gly Arg Ala Met Asn Cys Lys Ile Gly Ser
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 Phe Gln Leu Pro Pro Ala Ala Leu Gly Thr Phe Asp Thr Ala Ser Val
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 405 410 415
 Lys Phe Thr Gly Val Asp Lys Gly Phe Thr Glu Ile Gln Arg Met Gly
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 Ile Gly Leu Phe Val Ser Val Leu Cys Met Ala Ala Ala Ala Ile Val
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 Glu Ile Ile Arg Leu His Met Ala Asn Asp Leu Gly Leu Val Glu Ser
 450 455 460

Gly Ala Pro Val Pro Ile Ser Val Leu Trp Gln Ile Pro Gln Tyr Phe
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 Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe Ile Gly Gln Leu Glu Phe
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 Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg Ser Leu Cys Ser Ala Leu
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 Ala Leu Leu Thr Asn Ala Leu Gly Asn Tyr Leu Ser Ser Leu Ile Leu
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 Thr Leu Val Thr Tyr Phe Thr Thr Arg Asn Gly Gln Glu Gly Trp Ile
 530 535 540
 Ser Asp Asn Leu Asn Ser Ser Gly His Leu Asp Tyr Phe Phe Trp Leu Leu
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 Leu Val Phe Arg Ser Ser Leu Ala Gly Asp Asp Gly Thr Ser Gly Gly
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 ggt ctt agc gga ttc gtc ggg aag att aac tct agt atc cgt agc tct 148
 Gly Leu Ser Gly Phe Val Gly Lys Ile Asn Ser Ser Ile Arg Ser Ser
 30 35 40
 cga att ggg ctc ttt tct aag ccg cct cca ggg ctt cct gct cct aga 196
 Arg Ile Gly Leu Phe Ser Lys Pro Pro Pro Gly Leu Pro Ala Pro Arg
 45 50 55
 aaa gaa gaa gcg ccg tcg att cgg tgg agg aaa ggg gaa tta atc ggt 244
 Lys Glu Glu Ala Pro Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly
 60 65 70 75
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Cys	Gly	Ala	Phe	Gly	Arg	Val	Tyr	Met	Gly	Met	Asn	Leu	Asp	Ser	Gly		
				80					85					90			
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Glu	Leu	Leu	Ala	Ile	Lys	Gln	Val	Leu	Ile	Ala	Pro	Ser	Ser	Ala	Ser		
			95					100				105					
aag	gag	aag	act	cag	ggg	cac	atc	cga	gag	ctt	gag	gaa	gaa	gta	caa	388	
Lys	Glu	Lys	Thr	Gln	Gly	His	Ile	Arg	Glu	Leu	Glu	Glu	Glu	Val	Gln		
		110					115					120					
ctt	ctt	aag	aat	ctt	tca	cat	ccg	aac	atc	gtt	aga	tac	ttg	ggg	act	436	
Leu	Leu	Lys	Asn	Leu	Ser	His	Pro	Asn	Ile	Val	Arg	Tyr	Leu	Gly	Thr		
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Val	Arg	Glu	Ser	Asp	Ser	Leu	Asn	Ile	Leu	Met	Glu	Phe	Val	Pro	Gly		
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Gly	Ser	Ile	Ser	Ser	Leu	Leu	Glu	Lys	Phe	Gly	Ser	Phe	Pro	Glu	Pro		
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Val	Ile	Ile	Met	Tyr	Thr	Lys	Gln	Leu	Leu	Leu	Gly	Leu	Glu	Tyr	Leu		
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His	Asn	Asn	Gly	Ile	Met	His	Arg	Asp	Ile	Lys	Gly	Ala	Asn	Ile	Leu		
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gtc	gat	aac	aaa	ggg	tgc	atc	aga	ctc	gca	gat	ttt	ggg	gct	tcc	aag	676	
Val	Asp	Asn	Lys	Gly	Cys	Ile	Arg	Leu	Ala	Asp	Phe	Gly	Ala	Ser	Lys		
	205					210					215						
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Lys	Val	Val	Glu	Leu	Ala	Thr	Val	Asn	Gly	Ala	Lys	Ser	Met	Lys	Gly		
	220				225					230					235		
acg	cct	tat	tgg	atg	gct	cct	gaa	gtc	att	ctc	cag	act	ggg	cat	agc	772	
Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	Val	Ile	Leu	Gln	Thr	Gly	His	Ser		
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ttc	tct	gct	gat	ata	tgg	agt	gtt	ggg	tgc	act	gtg	att	gag	atg	gct	820	
Phe	Ser	Ala	Asp	Ile	Trp	Ser	Val	Gly	Cys	Thr	Val	Ile	Glu	Met	Ala		
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Thr	Gly	Lys	Pro	Pro	Trp	Ser	Glu	Gln	Tyr	Gln	Gln	Phe	Ala	Ala	Val		
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Leu	His	Ile	Gly	Arg	Thr	Lys	Ala	His	Pro	Pro	Ile	Pro	Glu	Asp	Leu		
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Gly Lys Arg Gln Glu 335	Pro Tyr Pro Ala Tyr Arg Asn Ser 340	Leu Thr Glu 345		
tgt gga aac cca ata act act caa gga atg aat gtt cgg agt tca ata				1108
Cys Gly Asn Pro Ile Thr Thr 350	Gln Gly Met Asn Val Arg Ser Ser Ile 355			
aat tcg ttg atc agg agg tcg aca tgt tca ggc ttg aag gat gtc tgt				1156
Asn Ser Leu Ile Arg Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys 365				
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Glu Leu Gly Ser Leu Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn 380				
aac tca gga ttt ggt tgg cga gat gga gac tct gat gac ctt tgt cag				1252
Asn Ser Gly Phe Gly Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln 400				
acc gat atg gat gat ctc tgc aac att gaa tca gtc aga aac aat gtt				1300
Thr Asp Met Asp Asp Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val 415				
ttg tca cag tcc acc gat tta aac aag agt ttt aat ccc atg tgt gat				1348
Leu Ser Gln Ser Thr Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp 430				
tcc acg gat aac tgg tct tgc aag ttt gat gaa agc cca aaa gtg atg				1396
Ser Thr Asp Asn Trp Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met 445				
aaa agc aaa tct aac ctg ctt tct tac caa gct tct caa ctc caa act				1444
Lys Ser Lys Ser Asn Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr 460				
gga gtt cca tgt gat gag gaa acc agc tta aca ttt gct ggt ggc tct				1492
Gly Val Pro Cys Asp Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser 480				
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Ser Val Ala Glu Asp Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser 495				
ttt ttg gat gag aag gct cag gat ttg aaa agg ttg cag acc cct ctg				1588
Phe Leu Asp Glu Lys Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu 510				
ctt gaa gaa ttc cac aat gct atg aat cca gga ata ccc caa ggt gca				1636
Leu Glu Glu Phe His Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala 525				

ctt gga gac acc aat atc tac aat tta cca aac tta cca agt ata agc 1684
 Leu Gly Asp Thr Asn Ile Tyr Asn Leu Pro Asn Leu Pro Ser Ile Ser
 540 545 550 555
 aag aca cct aaa cga ctt ccg agt aga cga ctc tca gca atc agt gat 1732
 Lys Thr Pro Lys Arg Leu Pro Ser Arg Arg Leu Ser Ala Ile Ser Asp
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 gct atg ccc agc cca ctc aaa agc tcc aaa cgt aca ctg aac aca agc 1780
 Ala Met Pro Ser Pro Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser
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 Ser Lys Pro Pro Pro Gly Leu Pro Ala Pro Arg Lys Glu Glu Ala Pro
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 Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly Cys Gly Ala Phe Gly
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 Arg Val Tyr Met Gly Met Asn Leu Asp Ser Gly Glu Leu Leu Ala Ile
 85 90 95

Lys Gln Val Leu Ile Ala Pro Ser Ser Ala Ser Lys Glu Lys Thr Gln
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 Gly His Ile Arg Glu Leu Glu Glu Val Gln Leu Leu Lys Asn Leu
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 Ser His Pro Asn Ile Val Arg Tyr Leu Gly Thr Val Arg Glu Ser Asp
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 Ser Leu Asn Ile Leu Met Glu Phe Val Pro Gly Gly Ser Ile Ser Ser
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 Leu Leu Glu Lys Phe Gly Ser Phe Pro Glu Pro Val Ile Ile Met Tyr
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 Thr Lys Gln Leu Leu Leu Gly Leu Glu Tyr Leu His Asn Asn Gly Ile
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 Met His Arg Asp Ile Lys Gly Ala Asn Ile Leu Val Asp Asn Lys Gly
 195 200 205
 Cys Ile Arg Leu Ala Asp Phe Gly Ala Ser Lys Lys Val Val Glu Leu
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 Ala Thr Val Asn Gly Ala Lys Ser Met Lys Gly Thr Pro Tyr Trp Met
 225 230 235 240
 Ala Pro Glu Val Ile Leu Gln Thr Gly His Ser Phe Ser Ala Asp Ile
 245 250 255
 Trp Ser Val Gly Cys Thr Val Ile Glu Met Ala Thr Gly Lys Pro Pro
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 Trp Ser Glu Gln Tyr Gln Gln Phe Ala Ala Val Leu His Ile Gly Arg
 275 280 285
 Thr Lys Ala His Pro Pro Ile Pro Glu Asp Leu Ser Pro Glu Ala Lys
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 Asp Phe Leu Met Lys Cys Leu His Lys Glu Pro Ser Leu Arg Leu Ser
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 Ala Thr Glu Leu Leu Gln His Pro Phe Val Thr Gly Lys Arg Gln Glu
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 Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu Cys Gly Asn Pro Ile
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Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln Thr Asp Met Asp Asp
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 Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser Phe Leu Asp Glu Lys
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Arg	Val	Ala	Gly	Glu	Gly	Gly	Leu	Asp	Thr	Thr	Pro	Pro	Pro	Pro	Pro	
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Pro	Thr	Ala	Asp	Thr	Val	Val	Ala	Gly	Arg	Thr	Ser	Leu	Gly	Glu	Ala	
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Pro	Pro	Pro	Arg	Gln	Pro	Pro	Arg	Pro	Pro	Thr	Ala	Arg	Trp	Ser	Ala	
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Met	Gly	Arg	Val	Met	Cys	Ser	Pro	Pro	Ile	Pro	Leu	Ser	Arg	Ser	Arg	
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cta	gcg	ctt	gac	gac	caa	cgt	tgg	ccg	gat	tgg	aca	acg	aac	ggt	tgg	336
Leu	Ala	Leu	Asp	Asp	Gln	Arg	Trp	Pro	Asp	Trp	Thr	Thr	Asn	Gly	Trp	
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cta	agc	atg	aga	ccg	acg	tcc	tcg	cca	aca	agg	cga	att	gac	cca	caa	384
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Gly	Ala	Arg	Arg	Ser	Ser	Val	Ser	Pro	Ala	Pro	Val	Thr	Thr	Gly	Met	
	130					135					140					
gcc	acc	tct	cgc	act	gac	gat	acg	cta	ata	gag	gca	gag	acc	ggt	cgc	480
Ala	Thr	Ser	Arg	Thr	Asp	Asp	Thr	Leu	Ile	Glu	Ala	Glu	Thr	Gly	Arg	
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gac	tgg	acg	agg	aaa	cga	atg	gtc	agg	aaa	ttg	ctt	aaa	gca	agg	gcg	528
Asp	Trp	Thr	Arg	Lys	Arg	Met	Val	Arg	Lys	Leu	Leu	Lys	Ala	Arg	Ala	
				165					170					175		
aaa	gac	tac	aag	gag	ggg	gga	att	gcg	gca	tac	ttt	ggt	tta	cga	gtg	576
Lys	Asp	Tyr	Lys	Glu	Gly	Gly	Ile	Ala	Ala	Tyr	Phe	Gly	Leu	Arg	Val	
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ctg	cga	tgc	tac	tcg	agg	atc	gta	cga	tcg	atg	aaa	cgc	cca	ggc	aac	624
Leu	Arg	Cys	Tyr	Ser	Arg	Ile	Val	Arg	Ser	Met	Lys	Arg	Pro	Gly	Asn	
		195					200					205				
ttg	aaa	ttc	acg	tgc	cgg	agg	gat	gtg	gca	ata	gcc	acg	ttc	agc	ggc	672
Leu	Lys	Phe	Thr	Cys	Arg	Arg	Asp	Val	Ala	Ile	Ala	Thr	Phe	Ser	Gly	

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ctc gtg tcc gcg ggc cag agc gtg gcg tca ttc tgc ctt ttc ctg ata Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile 245 250 255			768
tgc acg gcg ccc tcg gcg atg cgg ctg gtt agc ctt ctt aca ctg acc Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr 260 265 270			816
cca agc atg acc tac cta aca tgc ggg ctg gga tgg atg acc gtc gtc Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val 275 280 285			864
gta ctg ccg gcg ata gtg gtc cac tgt tat atg cgc cga cat acg gaa Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu 290 295 300			912
ggg gga tgg ccg tat gcg gca ctc gag gag cat aag acg gag ccg gga Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly 305 310 315 320			960
cga aat gaa aag atc acc ccg agt aga cgc aac tcg gcg ttc ggc ggc Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly 325 330 335			1008
ctg gtc ggt cga aat aaa aga cga aag aag tcc aag gtc tcc ggc gca Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala 340 345 350			1056
ccg aca gcg gtt tac aca gcg atg ttt ttc atg ttc tcc acg gca atc Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile 355 360 365			1104
aag ggg atg gtg gtg tgc aca atg aaa aaa aaa gtc aaa aaa agt gcg Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala 370 375 380			1152
aat cgc aga ctc cgc cag ttg ctc cga tgg gcg cga tac cac gcg aac Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn 385 390 395 400			1200
gcg ttc ttg ctc tgt tct ctt gca tgc gca cga ttc gcg gca tcg cga Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg 405 410 415			1248
acg gtc atc cat tgc agt att tac cca cgt ttc ggc ccc tta gcc acg Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr 420 425 430			1296
gtg acg gcc ata tgt ttg ata cta cac acg tgt acg tac cga cgt acg Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr 435 440 445			1344

gag gca gac acg acg cga cac gaa aat gac gac gcc cgg aag gtg atg 1392
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
 450 455 460
 gaa gac atg gcc aaa cga atg gac gat agt agc agt ggg agc acg ttg 1440
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
 465 470 475 480
 agc acg ctc acg act gac gag acg tac cac acc acc acg gag gtg acc 1488
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
 485 490 495
 gat ttt gat tca tct cca tcg tgg gga cga tgc tca tcg cgg cgc ccg 1536
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro
 500 505 510
 ccg gcg ctg ctg gaa tcg aca ttt cgg cga tcc ccg aga ggg tcg acg 1584
 Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr
 515 520 525
 gga cga cga tgg cga gag tag attcggagtc aggaacgttg gaccgacagg 1635
 Gly Arg Arg Trp Arg Glu 530 535
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 35 40 45
 Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala
 50 55 60
 Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala
 65 70 75 80
 Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg
 85 90 95
 Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp
 100 105 110

Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln
 115 120 125
 Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met
 130 135 140
 Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg
 145 150 155 160
 Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala
 165 170 175
 Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val
 180 185 190
 Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn
 195 200 205
 Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly
 210 215 220
 Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser
 225 230 235 240
 Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile
 245 250 255
 Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr
 260 265 270
 Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val
 275 280 285
 Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu
 290 295 300
 Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly
 305 310 315 320
 Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly
 325 330 335
 Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala
 340 345 350
 Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile
 355 360 365
 Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala
 370 375 380
 Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn
 385 390 395 400
 Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg
 405 410 415

Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr
 420 425 430
 Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr
 435 440 445
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
 450 455 460
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
 465 470 475 480
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
 485 490 495
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro
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 Ala Lys Lys Gly Ala Asn Leu Phe Lys
 15 20
 ccgctgaaaa ttctcagggc gcattctatc ccgcagaact tttctgacca cttttagtag 155
 acc cgc tgc gct cag tgc cac acc ctg aag gcc ggc gag ggc aac aag 203
 Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly Glu Gly Asn Lys
 25 30 35

att ggc cct gag ctc cac ggt ctc ttc ggc cgc aag act ggt tcc gtc 251
 Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys Thr Gly Ser Val
 40 45 50

gct ggc tac tca tac acc gac gcc aac aag cag aag ggt atc gag tgg 299
 Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys Gly Ile Glu Trp
 55 60 65

aag gac gac act ctc gtacgtcacg ccaccggaag attgaaatgt ccccgagacc 354
 Lys Asp Asp Thr Leu
 70

ctccgctaac acgacacag ttc gag tac ctc gag aac ccc aag aag tac att 406
 Phe Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile
 75 80

ccc ggt acc aag atg gcc ttc ggt ggt ctc aag aag ccc aag gac cgc 454
 Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys Pro Lys Asp Arg
 85 90 95 100

aac gac ctc atc acc ttc ctt gag gag gag acc aaa taa gcgtcttgct 503
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 105 110

acccc 508

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 35 40 45

Thr Gly Ser Val Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys
 50 55 60

Gly Ile Glu Trp Lys Asp Asp Thr Leu Phe Glu Tyr Leu Glu Asn Pro
 65 70 75 80

Lys Lys Tyr Ile Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys
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 tta atc aga act cca caa aca aaa caa cgt ctc aat ttc cac tca aaa 96
 Leu Ile Arg Thr Pro Gln Thr Lys Gln Arg Leu Asn Phe His Ser Lys
 20 25 30
 acc cca aac cca gac gga tct aaa gat cca tct cca ccg gag cat cca 144
 Thr Pro Asn Pro Asp Gly Ser Lys Asp Pro Ser Pro Pro Glu His Pro
 35 40 45

78

His Cys Ile
255

atgcagctta tctctgtttt aacttactag tgtgggttgtt tctttttgta g atc ata 938
Ile Ile

ctt gat gtg cca act gtt ggg gga aga ttg atg ctt gtt gac atg gct 986
Leu Asp Val Pro Thr Val Gly Gly Arg Leu Met Leu Val Asp Met Ala
260 265 270

ggg tct gaa aat ata gac caa gct ggg cag act gga ttt gaa gct aag 1034
Gly Ser Glu Asn Ile Asp Gln Ala Gly Gln Thr Gly Phe Glu Ala Lys
275 280 285

atg caa gtaatgtttc ctctctcaat ttgtttgatt ctactaaagt tattgtagtt 1090
Met Gln
290

atggatatca actgacttat atctctcatt attcaacag act gct aag atc aac 1144
Thr Ala Lys Ile Asn
295

cag gga aat att gca ctg aag cga gtt gtg gaa tct ata gca aat gga 1192
Gln Gly Asn Ile Ala Leu Lys Arg Val Val Glu Ser Ile Ala Asn Gly
300 305 310

gat tct cat gta ccc ttt aga gac agc aag ctg acc atg ctt ctc cag 1240
Asp Ser His Val Pro Phe Arg Asp Ser Lys Leu Thr Met Leu Leu Gln
315 320 325

gtgaaattct tgttccattg ttttatcttc tggaaaatgt tttacgtgtt gcttggtttt 1300

cttgaagata tttagtgttg tttctattct ctgaatgcag gac tct ttt gaa gat 1355
Asp Ser Phe Glu Asp
330

gac aag tca aag att cta atg atc ctg tgt gcg agc ccg gat cca aag 1403
Asp Lys Ser Lys Ile Leu Met Ile Leu Cys Ala Ser Pro Asp Pro Lys
335 340 345

gaa atg cac aag act ctc tgt act cta gag tat ggg gca aaa gca aag 1451
Glu Met His Lys Thr Leu Cys Thr Leu Glu Tyr Gly Ala Lys Ala Lys
350 355 360 365

tgc ata gtt cgt ggg tct cat act cca aac aaa gat aag tat ggg ggt 1499
Cys Ile Val Arg Gly Ser His Thr Pro Asn Lys Asp Lys Tyr Gly Gly
370 375 380

gat gag tct gct tct gct gtg att ttg gga tca aga ata gct gcc atg 1547
Asp Glu Ser Ala Ser Ala Val Ile Leu Gly Ser Arg Ile Ala Ala Met
385 390 395

gat gag ttc att atc aaa ctc cag tct gag aag aag caa aaa gaa aaa 1595
Asp Glu Phe Ile Ile Lys Leu Gln Ser Glu Lys Lys Gln Lys Glu Lys
400 405 410

gaa agg aat gag gca caa aag cag ctg aag aag aag gaa gag gaa gtt 1643

71

Glu Arg Asn Glu Ala Gln Lys Gln Leu Lys Lys Lys Glu Glu Glu Val	
415 420 425	
gct gct tta aga tct ctt tta aca cag agg gaa gct tgt gct acc aat	1691
Ala Ala Leu Arg Ser Leu Leu Thr Gln Arg Glu Ala Cys Ala Thr Asn	
430 435 440 445	
gaa gag gag ata aaa gag aaa gta aac gag aga acc cag ctt ttg aag	1739
Glu Glu Glu Ile Lys Glu Lys Val Asn Glu Arg Thr Gln Leu Leu Lys	
450 455 460	
tcg gaa cta gat aag aaa ctt gaa gaa tgc cga aga atg gct gag gaa	1787
Ser Glu Leu Asp Lys Lys Leu Glu Glu Cys Arg Arg Met Ala Glu Glu	
465 470 475	
ttt gtt gag atg gag aga agg aga atg gag gaa agg ata gtt cag cag	1835
Phe Val Glu Met Glu Arg Arg Arg Met Glu Glu Arg Ile Val Gln Gln	
480 485 490	
caa gag gaa ctg gag atg atg agg aga cgg tta gag gaa atc gag gtt	1883
Gln Glu Glu Leu Glu Met Met Arg Arg Arg Leu Glu Glu Ile Glu Val	
495 500 505	
gag ttc cgc cgc tca aat gga gga agt gtt gat gaa act agt ggg ttt	1931
Glu Phe Arg Arg Ser Asn Gly Gly Ser Val Asp Glu Thr Ser Gly Phe	
510 515 520 525	
gcc aaa aga ctc agg agt ctt tac tct gat gat gat cct ggt atg gtg	1979
Ala Lys Arg Leu Arg Ser Leu Tyr Ser Asp Asp Asp Pro Gly Met Val	
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aag tca atg gac ctt gac atg ggt gat cca gaa cct gtc aag caa gtg	2027
Lys Ser Met Asp Leu Asp Met Gly Asp Pro Glu Pro Val Lys Gln Val	
545 550 555	
tgg gga gct gtt tca cac caa tca agc aac act att agt agc aac ttc	2075
Trp Gly Ala Val Ser His Gln Ser Ser Asn Thr Ile Ser Ser Asn Phe	
560 565 570	
act aac ctt ttg caa ccg aag cct tca gag aat atg ctt aca cag atg	2123
Thr Asn Leu Leu Gln Pro Lys Pro Ser Glu Asn Met Leu Thr Gln Met	
575 580 585	
tat cct gac cgg gta tgc ttg agc act gtc ttt gaa gaa gaa gaa gtt	2171
Tyr Pro Asp Arg Val Cys Leu Ser Thr Val Phe Glu Glu Glu Glu Val	
590 595 600 605	
gaa gaa gag gaa gaa aaa gtg ata gtc gag gat aaa agc atc tgc ttg	2219
Glu Glu Glu Glu Glu Lys Val Ile Val Glu Asp Lys Ser Ile Cys Leu	
610 615 620	
ata aca aca cca atg cct agt ttg aac tct gaa ggt ttg ggt aaa gag	2267
Ile Thr Thr Pro Met Pro Ser Leu Asn Ser Glu Gly Leu Gly Lys Glu	
625 630 635	
aac tgc ttc aac ggt gca gat gac aag gaa tca gcc tcg tct aga agg	2315
Asn Cys Phe Asn Gly Ala Asp Asp Lys Glu Ser Ala Ser Ser Arg Arg	

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tct caa cac agt gga cag gag gag gat caa gcc aat att gca tca cct Ser Gln His Ser Gly Gln Glu Glu Asp Gln Ala Asn Ile Ala Ser Pro 670 675 680 685			2411
gat aag aaa gac aat cag ttc ttt tct att acg aat aag gcc gaa gca Asp Lys Lys Asp Asn Gln Phe Phe Ser Ile Thr Asn Lys Ala Glu Ala 690 695 700			2459
cta gca gta gaa gaa gca aag gaa aac aat atc tca gtc gat caa agg Leu Ala Val Glu Glu Ala Lys Glu Asn Asn Ile Ser Val Asp Gln Arg 705 710 715			2507
gaa aac ggt cag cta gat atc tat gtt aaa tgg gaa aca gct gct gat Glu Asn Gly Gln Leu Asp Ile Tyr Val Lys Trp Glu Thr Ala Ala Asp 720 725 730			2555
aac cct cga aag ctc ata aca aca ctg aga gtt aca aag gat gca aca Asn Pro Arg Lys Leu Ile Thr Thr Leu Arg Val Thr Lys Asp Ala Thr 735 740 745			2603
cta gct gac ttg agg aag ctt att gag atc tac ctt gga tct gat aat Leu Ala Asp Leu Arg Lys Leu Ile Glu Ile Tyr Leu Gly Ser Asp Asn 750 755 760 765			2651
cag gct ttt acc ttt ctc aag ctc ggg gta ata aac ttg aac caa caa Gln Ala Phe Thr Phe Leu Lys Leu Gly Val Ile Asn Leu Asn Gln Gln 770 775 780			2699
gca caa aaa gct ttt cat ttt tat ctg ttt gttatgctct gatcctaaat Ala Gln Lys Ala Phe His Phe Tyr Leu Phe 785 790			2749
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aaa gaa tca aca gtt caa gct acg agc cta cct ctc tgc aac gga cac Lys Glu Ser Thr Val Gln Ala Thr Ser Leu Pro Leu Cys Asn Gly His 805 810 815			2849
gca tac ctc gcc act ttg aga cca gga aag agc tca caa cat aaa agt Ala Tyr Leu Ala Thr Leu Arg Pro Gly Lys Ser Ser Gln His Lys Ser 820 825 830			2897
ctt caa cct gca agc cca ctt cca ctt aat ccc ata gaa aac atg atg Leu Gln Pro Ala Ser Pro Leu Pro Leu Asn Pro Ile Glu Asn Met Met 835 840 845			2945
gaa gtt acc ccc atc tca aaa gtg aca ccg aac cat caa gttgatgaat Glu Val Thr Pro Ile Ser Lys Val Thr Pro Asn His Gln 850 855 860			2994

82

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Asp A

agctgcagat tcatagctct gtggaacccg ttgggttggt gcatgacgtg aaccacttga 4442

aaatagtcgg cttgagtggg tctcgcttgg ttcag ct gat gag cca ggt ctg gtg 4497
la Asp Glu Pro Gly Leu Val
925

ctt gat atc aca cct ctc ttt gag gtacttccat ttcgagactc gtgctgcaaa 4551
Leu Asp Ile Thr Pro Leu Phe Glu
930 935

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aatataagag acagagaaca tcaatgtacc tgtaggcttt tcagctcttt ctgcag gtg 5090
Val

gtc ctg gag ggt cca acg ctg gtc ttg gag ttg gct gtt gta aat gat 5138
Val Leu Glu Gly Pro Thr Leu Val Leu Glu Leu Ala Val Val Asn Asp
940 945 950

aga cac ata gca gga taa 5156
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955 960

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<211> 959

<212> PRT

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Val Glu Val Ile Gly Arg Ile Arg Asp Tyr Pro Asp Arg Lys Glu Lys

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Arg Ala Asp Val Gly Tyr Arg Asp Phe Thr Leu Asp Gly Val Ser Phe		
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Ser Glu Gln Glu Gly Leu Glu Glu Phe Tyr Lys Lys Phe Ile Glu Glu		
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Arg Ile Lys Gly Val Lys Val Gly Asn Lys Cys Thr Ile Met Met Tyr		
	115	120 125
Gly Pro Thr Gly Ala Gly Lys Ser His Thr Met Phe Gly Cys Gly Lys		
	130	135 140
Glu Pro Gly Ile Val Tyr Arg Ser Leu Arg Asp Ile Leu Gly Asp Ser		
	145	150 155 160
Asp Gln Asp Gly Val Thr Phe Val Gln Val Thr Val Leu Glu Val Tyr		
	165	170 175
Asn Glu Glu Ile Tyr Asp Leu Leu Ser Thr Asn Ser Ser Asn Asn Leu		
	180	185 190
Gly Ile Gly Trp Pro Lys Gly Ala Ser Thr Lys Val Arg Leu Glu Val		
	195	200 205
Met Gly Lys Lys Ala Lys Asn Ala Ser Phe Ile Ser Gly Thr Glu Ala		
	210	215 220
Gly Lys Ile Ser Lys Glu Ile Val Lys Val Glu Lys Arg Arg Ile Val		
	225	230 235 240
Lys Ser Thr Leu Cys Asn Glu Arg Ser Ser Arg Ser His Cys Ile Ile		
	245	250 255
Ile Leu Asp Val Pro Thr Val Gly Gly Arg Leu Met Leu Val Asp Met		
	260	265 270
Ala Gly Ser Glu Asn Ile Asp Gln Ala Gly Gln Thr Gly Phe Glu Ala		
	275	280 285
Lys Met Gln Thr Ala Lys Ile Asn Gln Gly Asn Ile Ala Leu Lys Arg		
	290	295 300
Val Val Glu Ser Ile Ala Asn Gly Asp Ser His Val Pro Phe Arg Asp		
	305	310 315 320
Ser Lys Leu Thr Met Leu Leu Gln Asp Ser Phe Glu Asp Asp Lys Ser		
	325	330 335
Lys Ile Leu Met Ile Leu Cys Ala Ser Pro Asp Pro Lys Glu Met His		
	340	345 350
Lys Thr Leu Cys Thr Leu Glu Tyr Gly Ala Lys Ala Lys Cys Ile Val		

355	360	365
Arg Gly Ser His Thr Pro Asn Lys Asp Lys Tyr Gly Gly Asp Glu Ser		
370	375	380
Ala Ser Ala Val Ile Leu Gly Ser Arg Ile Ala Ala Met Asp Glu Phe		
385	390	395
Ile Ile Lys Leu Gln Ser Glu Lys Lys Gln Lys Glu Lys Glu Arg Asn		
	405	410
Glu Ala Gln Lys Gln Leu Lys Lys Lys Glu Glu Glu Val Ala Ala Leu		
	420	425
Arg Ser Leu Leu Thr Gln Arg Glu Ala Cys Ala Thr Asn Glu Glu Glu		
	435	440
Ile Lys Glu Lys Val Asn Glu Arg Thr Gln Leu Leu Lys Ser Glu Leu		
	450	455
Asp Lys Lys Leu Glu Glu Cys Arg Arg Met Ala Glu Glu Phe Val Glu		
465	470	475
Met Glu Arg Arg Arg Met Glu Glu Arg Ile Val Gln Gln Gln Glu Glu		
	485	490
Leu Glu Met Met Arg Arg Arg Leu Glu Glu Ile Glu Val Glu Phe Arg		
	500	505
Arg Ser Asn Gly Gly Ser Val Asp Glu Thr Ser Gly Phe Ala Lys Arg		
	515	520
Leu Arg Ser Leu Tyr Ser Asp Asp Asp Pro Gly Met Val Lys Ser Met		
	530	535
Asp Leu Asp Met Gly Asp Pro Glu Pro Val Lys Gln Val Trp Gly Ala		
545	550	555
Val Ser His Gln Ser Ser Asn Thr Ile Ser Ser Asn Phe Thr Asn Leu		
	565	570
Leu Gln Pro Lys Pro Ser Glu Asn Met Leu Thr Gln Met Tyr Pro Asp		
	580	585
Arg Val Cys Leu Ser Thr Val Phe Glu Glu Glu Glu Val Glu Glu Glu		
	595	600
Glu Glu Lys Val Ile Val Glu Asp Lys Ser Ile Cys Leu Ile Thr Thr		
	610	615
Pro Met Pro Ser Leu Asn Ser Glu Gly Leu Gly Lys Glu Asn Cys Phe		
625	630	635
Asn Gly Ala Asp Asp Lys Glu Ser Ala Ser Ser Arg Arg Leu Arg Ile		
	645	650
Gln Asn Ile Phe Thr Leu Cys Gly Asn Gln Arg Glu Leu Ser Gln His		

660					665					670					
Ser	Gly	Gln	Glu	Glu	Asp	Gln	Ala	Asn	Ile	Ala	Ser	Pro	Asp	Lys	Lys
	675						680					685			
Asp	Asn	Gln	Phe	Phe	Ser	Ile	Thr	Asn	Lys	Ala	Glu	Ala	Leu	Ala	Val
	690					695					700				
Glu	Glu	Ala	Lys	Glu	Asn	Asn	Ile	Ser	Val	Asp	Gln	Arg	Glu	Asn	Gly
705					710					715					720
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Tyr Leu Met Phe Val Met Leu Met Gly Leu Gly Phe Thr Ile Ser Asn
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 Ile Ser Asn Cys Asn Val Leu Ala Phe Ser Gly Ile Lys Thr Ser Pro
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Gly	Phe	Ser	Val	Asp	Asn	Ala	Thr	Leu	Asn	Arg	Phe	Phe	Ser	Leu	His	
	175					180					185					
cat	tta	ctc	ccc	ttt	att	tta	gta	ggc	gcc	agt	ctt	ctt	cat	ctg	gcc	626
His	Leu	Leu	Pro	Phe	Ile	Leu	Val	Gly	Ala	Ser	Leu	Leu	His	Leu	Ala	
190					195					200					205	
gca	ttg	cat	caa	tat	gga	tca	aat	aat	cca	ttg	ggt	gta	cat	tct	gag	674
Ala	Leu	His	Gln	Tyr	Gly	Ser	Asn	Asn	Pro	Leu	Gly	Val	His	Ser	Glu	
			210						215					220		
atg	gat	aaa	ata	gct	ttt	tac	cct	tat	ttt	tat	gtc	aag	gat	cta	ggt	722
Met	Asp	Lys	Ile	Ala	Phe	Tyr	Pro	Tyr	Phe	Tyr	Val	Lys	Asp	Leu	Val	
			225					230					235			
ggt	tgg	gta	gct	ttt	gct	atc	ttt	ttt	tct	att	tgg	att	ttt	tat	gct	770
Gly	Trp	Val	Ala	Phe	Ala	Ile	Phe	Phe	Ser	Ile	Trp	Ile	Phe	Tyr	Ala	
		240				245						250				
cct	aat	ggt	ttg	gga	cat	ccc	gac	aat	tat	ata	cct	gct	aat	ccg	atg	818
Pro	Asn	Val	Leu	Gly	His	Pro	Asp	Asn	Tyr	Ile	Pro	Ala	Asn	Pro	Met	
	255					260					265					
tcc	acc	ccg	cct	cat	att	gtg	ccg	gaa	tgg	tat	ttc	cta	ccg	atc	cat	866
Ser	Thr	Pro	Pro	His	Ile	Val	Pro	Glu	Trp	Tyr	Phe	Leu	Pro	Ile	His	
270					275					280					285	
gcc	att	ctt	cgt	agt	ata	cct	gac	aaa	gcg	gga	ggt	gta	gcc	gca	ata	914
Ala	Ile	Leu	Arg	Ser	Ile	Pro	Asp	Lys	Ala	Gly	Gly	Val	Ala	Ala	Ile	

	290	295	300	
gca cca gtt ttt ata tgt ctc ttg gct tta cct ttt ttt aaa agt atg				962
Ala Pro Val Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met				
	305	310	315	
tat gtg cgt agt tca agt ttt cga ccg att cac caa gga atg ttt tgg				1010
Tyr Val Arg Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp				
	320	325	330	
ttg ctt ttg gcg gat tgc tta cta cta ggt tgg atc gga tgt caa cct				1058
Leu Leu Leu Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro				
	335	340	345	
gtg gag gct cca ttt gtt act att gga caa att tct cct ttg gtt ttc				1106
Val Glu Ala Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe				
	350	355	360	365
ttc ttg ttc ttt gcc ata acg ccc att ctg gga cga gtt gga aga gga				1154
Phe Leu Phe Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly				
	370	375	380	
att cct aat tct tac acg gat gag act gat cac acc tga tcagtgaaaa				1203
Ile Pro Asn Ser Tyr Thr Asp Glu Thr Asp His Thr				
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<211> 393

<212> PRT

<213> Arabidopsis thaliana

<400> 46

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	20	25	30	
Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys Leu Val Ile				
	35	40	45	
Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr Pro His Val				
	50	55	60	
Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp Val Glu Gly				
	65	70	75	80
Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser Met Phe Leu				
	85	90	95	
Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His Ala Ser Tyr				
	100	105	110	
Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val Ile Phe Leu				
	115	120	125	

Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro Trp Gly Gln
 130 135 140
 Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala Ser Ala Ile
 145 150 155 160
 Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly Gly Phe Ser
 165 170 175
 Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His His Leu Leu
 180 185 190
 Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala Ala Leu His
 195 200 205
 Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu Met Asp Lys
 210 215 220
 Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val Gly Trp Val
 225 230 235 240
 Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala Pro Asn Val
 245 250 255
 Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met Ser Thr Pro
 260 265 270
 Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His Ala Ile Leu
 275 280 285
 Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile Ala Pro Val
 290 295 300
 Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met Tyr Val Arg
 305 310 315 320
 Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp Leu Leu Leu
 325 330 335
 Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro Val Glu Ala
 340 345 350
 Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe Phe Leu Phe
 355 360 365
 Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly Ile Pro Asn
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 Ser Tyr Thr Asp Glu Thr Asp His Thr
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<212> DNA

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cga gga aat tac gca gct aca ctc gat gtg tcg tat ccg gta ttc ccg	96
Arg Gly Asn Tyr Ala Ala Thr Leu Asp Val Ser Tyr Pro Val Phe Pro	
20 25 30	
caa aat aaa gat ggc cgt gca ctt cag aaa gtt ctc gga acc att cgt	144
Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg	
35 40 45	
aac gga gat ttg gct gtt tcg gct cct aaa aca agt ctt agg gca ggt	192
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly	
50 55 60	
att ttc ggt gaa ggt tcc agc ttg gtc gat cag atg ccc tgt aaa gtt	240
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val	
65 70 75 80	
tac gtg gcg ttc cac aaa gaa tca tac tgc tcg ctt acc ggg cta agc	288
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser	
85 90 95	
aaa cgc gga gtc gca ata aac gaa gca agt ctt tcc ctg gtc gga atc	336
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile	
100 105 110	
act aaa gtt aga gcc ccc gtc gga aat acc gtt gga gcg gaa gca acc	384
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr	
115 120 125	
gta tac ata ggt agt cca aaa cct tat aca gag tgt agt act cca aat	432
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn	
130 135 140	
aaa atg tat gcg gtt gca gct ggt ttc aag gtg gca agt ttc gcc gct	480
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala	
145 150 155 160	
agt acg tgc gta cgt ccg cct gca cgt gca cgt cgt acg ctg acc gtg	528
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val	
165 170 175	
acg tcg acc gtg acg ctg tct atg gca act ggt aaa tgc gta aat aca	576
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr	
180 185 190	
gga aac gaa cca gta tct aaa cct aca gga gta cgt atg atg tta att	624
Gly Asn Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile	
195 200 205	

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cct ctc gat gct act ctc att aaa gta tgg act ggg gaa gta aaa aaa 672
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys
210 215 220

gcg ata gtt tcc cgg cct gca aaa att ttc aat agc gta gga aat tta 720
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu
225 230 235 240

gaa cgt cct tca att tcg cat tct tgt gga caa ggt ttg gat gaa gct 768
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala
245 250 255

gcc gct tat atc aag ggt aga ctt tct cca atc gtt aaa gca gaa aga 816
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg
260 265 270

att aaa gtt ttg gtt aaa gac gag cac gaa gaa gta aaa gaa ctt ctt 864
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu
275 280 285

caa gaa ggt tac gaa gaa atc gtc ggt gag tct cca agt ttc aat tta 912
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu
290 295 300

gca caa gaa gcg tgg gaa aaa gct gaa aga cga gca aaa ggt cag tcc 960
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser
305 310 315 320

ccg tgc agt gcg gca aaa gca aac ctt gca acc tac tat ttt tca aca 1008
Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
325 330 335

ggt gat ttc gaa aaa tca att aaa ctc tac gaa gaa cct atg ggt ttg 1056
Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
340 345 350

aaa gat act gat aag agc tat ctg cga gaa cgt aga aaa aga gta gag 1104
Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
355 360 365

gct act acg ttg cgt gca ccg ttc gtg gtc cag ctg acc gtg cgt agt 1152
Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
370 375 380

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<211> 397

<212> PRT

<213> Arabidopsis thaliana

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Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly	50	55	60
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val	65	70	75
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser	85	90	95
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile	100	105	110
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr	115	120	125
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn	130	135	140
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala	145	150	155
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val	165	170	175
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr	180	185	190
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile	195	200	205
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys	210	215	220
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu	225	230	235
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala	245	250	255
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg	260	265	270
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu	275	280	285
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu	290	295	300
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser			

305 310 315 320
 Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
 325 330 335
 Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
 340 345 350
 Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
 355 360 365
 Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
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 385 390 395

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 gtc gtc ttt tcc gtc gcg ctt ctt ctg ttc tac ttc tct gaa act tct 97
 Val Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser
 20 25 30
 cta gga gct cct tgt ccc atc aat ggc ttg cca atc gtg agg aat att 145
 Leu Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile
 35 40 45
 agt gac ctt cct cag gat aac tat gga aga cca ggt ctt tcc cac atg 193
 Ser Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met
 50 55 60
 act gtt gct ggc tcc gta ttg cat gga atg aaa gag gtt gaa ata tgg 241
 Thr Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp
 65 70 75
 ctt cag aca ttt gct cca ggt tca gag aca cca att cac agg cac tcc 289
 Leu Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser
 80 85 90 95
 tgt gaa gag gtt ttt gtt gtc cta aag ggc agt ggt act ctg tat ctc 337
 Cys Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu
 100 105 110

gct gaa aca cat gga aat ttc cct ggg aaa cca atc gaa ttt cca atc 385
 Ala Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile
 115 120 125

ttt gcc aac agt aca att cat att ccg atc aat gat gct cat cag gtc 433
 Phe Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val
 130 135 140

aaa aac acc ggt cat gag gac ctg cag gtg ttg gtt atc ata tct cgg 481
 Lys Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg
 145 150 155

ccg cct att aaa atc ttc atc tac gaa gac tgg ttt atg cca cac act 529
 Pro Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr
 160 165 170 175

gct gca agg ctg aag ttc cct tac tat tgg gat gag caa tgc att caa 577
 Ala Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln
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gaa tca caa aaa gac gag ctt taa agcaaagtcc 611
 Glu Ser Gln Lys Asp Glu Leu
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<210> 50
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 <213> Arabidopsis thaliana

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Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile Ser
 35 40 45

Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met Thr
 50 55 60

Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp Leu
 65 70 75 80

Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser Cys
 85 90 95

Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala
 100 105 110

Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe
 115 120 125

Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val Lys
 130 135 140

Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg Pro
 145 150 155 160
 Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr Ala
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 Ser Gln Lys Asp Glu Leu
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 Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Arg Pro
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 acc gct atc ctt atc gga acc ctc acc gct tta ggc ggt gga gtt aga 144
 Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg
 35 40 45
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 Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala
 50 55 60
 ata gcg cgt gat agc tgt gcc gtg ttc gca tgg aag cga ggt acg cga 240
 Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg
 65 70 75 80
 caa gag tac tgg tgc tcg act gaa ccg acc ctt gac tgg ggc ccc ggt 288
 Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly
 85 90 95
 ggt gga ccc gac ttc gat tgt gat gat ggt ggt gac gat ccg ctt ttg 336
 Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu
 100 105 110
 att caa gat ggc gta aaa gct gcg gag gaa tat gct aaa tct gga aaa 384
 Ile Gln Asp Gly Val Lys Ala Ala Glu Glu Tyr Ala Lys Ser Gly Lys
 115 120 125

gtt cca gat cca agc tgt act gat aat gct gag ttt caa gtt gtg ctt	432
Val Pro Asp Pro Ser Cys Thr Asp Asn Ala Glu Phe Gln Val Val Leu	
130 135 140	
att att att agg gag ggg ttg aaa act gat cct tta aaa tac act aag	480
Ile Ile Ile Arg Glu Gly Leu Lys Thr Asp Pro Leu Lys Tyr Thr Lys	
145 150 155 160	
cga ccc agt tgc ctt gtt ggt gtt tct gag gaa act act act ggt gtt	528
Arg Pro Ser Cys Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val	
165 170 175	
aag aga agt tac caa atg cag ccg aaa tgt act ttg ctt ttg cat gct	576
Lys Arg Ser Tyr Gln Met Gln Pro Lys Cys Thr Leu Leu Leu His Ala	
180 185 190	
act gat gtt tgt gac acc gtg atc aag agc aag att gat aac ttg tac	624
Thr Asp Val Cys Asp Thr Val Ile Lys Ser Lys Ile Asp Asn Leu Tyr	
195 200 205	
gga tgc cgc cac tca ctt tcg gat ggt ctc atg agg gct act gat gtt	672
Gly Cys Arg His Ser Leu Ser Asp Gly Leu Met Arg Ala Thr Asp Val	
210 215 220	
cgt cgc ccc tgc aag gta gcg ctt gta ggc ggt tac gga gat gtc ttt	720
Arg Arg Pro Cys Lys Val Ala Leu Val Gly Gly Tyr Gly Asp Val Phe	
225 230 235 240	
aag ggt tgg gtt gct gcc ttg aag caa gct ggt gca cgt gtc atc gtg	768
Lys Gly Trp Val Ala Ala Leu Lys Gln Ala Gly Ala Arg Val Ile Val	
245 250 255	
act gag atc ccg caa atc tgt gcc gtc caa gct acc atg gaa ggt agt	816
Thr Glu Ile Pro Gln Ile Cys Ala Val Gln Ala Thr Met Glu Gly Ser	
260 265 270	
tcg gtc ctt acc ctt gag gat gtc gtt tca gat gtt gat cgc ttc gtt	864
Ser Val Leu Thr Leu Glu Asp Val Val Ser Asp Val Asp Arg Phe Val	
275 280 285	
acg aca acc ggt aac aag gac ctc atc atg gtt gac cac atg agg cga	912
Thr Thr Thr Gly Asn Lys Asp Leu Ile Met Val Asp His Met Arg Arg	
290 295 300	
atg aag aac cag gcc ata gtt tgc aac att cga cgt ttc gac aat gaa	960
Met Lys Asn Gln Ala Ile Val Cys Asn Ile Arg Arg Phe Asp Asn Glu	
305 310 315 320	
atc gac atg cgc agt ctc gag acc ttc cct gga gtg aag cgg atc aca	1008
Ile Asp Met Arg Ser Leu Glu Thr Phe Pro Gly Val Lys Arg Ile Thr	
325 330 335	
atc aag gcc cag act gac aga tgg gtc ttt cgc gac acc aac aga ggt	1056
Ile Lys Ala Gln Thr Asp Arg Trp Val Phe Arg Asp Thr Asn Arg Gly	
340 345 350	
atc att gtc cca gcc gag ggg cgt ctc atg acg atg gga tgc gcc act	1104

Ile Ile Val Pro Ala Glu Gly Arg Leu Met Thr Met Gly Cys Ala Thr
 355 360 365

gga cac ccc agc ttc cgg acg tcc tgc tct ttc act aac caa gtc agt 1152
 Gly His Pro Ser Phe Arg Thr Ser Cys Ser Phe Thr Asn Gln Val Ser
 370 375 380

tct cag ctc gag ttg tgg cgg gag aag agc acc ggc aag tat gag aag 1200
 Ser Gln Leu Glu Leu Trp Arg Glu Lys Ser Thr Gly Lys Tyr Glu Lys
 385 390 395 400

aaa gtg tac gtc ttc cca aag cac ctt gag aag aag gtt gcc gcc ctt 1248
 Lys Val Tyr Val Phe Pro Lys His Leu Glu Lys Lys Val Ala Ala Leu
 405 410 415

cat ctc gta aag ctc gga gca agg ctc act aag ctt agt cgg tgc acg 1296
 His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr
 420 425 430

ttg ttg tgc acg gac gac cca gtt gaa ggt cgt aaa gag cct cct cac 1344
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 435 440 445

cgt gct ggc agc cct gaa ccg tgc cag ctg cag ctg acc gtg ttc agg 1392
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tag taa 1398
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 <213> Arabidopsis thaliana

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 35 40 45

Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala
 50 55 60

Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg
 65 70 75 80

Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly
 85 90 95

Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu

105

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gac	gtc	gat	gaa	att	gtc	agg	tta	agg	aag	agg	ttt	ttc	aag	ttg	gac	96
Asp	Val	Asp	Glu	Ile	Val	Arg	Leu	Arg	Lys	Arg	Phe	Phe	Lys	Leu	Asp	
			20					25					30			
aga	gat	tgt	tca	gga	tca	gaa	ctt	gga	agt	gag	ttc	atg	agt	ttg	cct	144
Arg	Asp	Cys	Ser	Gly	Ser	Glu	Leu	Gly	Ser	Glu	Phe	Met	Ser	Leu	Pro	
		35					40					45				
caa	gtt	agt	tcg	aac	cct	ctt	cgg	atg	cgt	gag	atg	cgt	aat	ttc	gat	192
Gln	Val	Ser	Ser	Asn	Pro	Leu	Arg	Met	Arg	Glu	Met	Arg	Asn	Phe	Asp	
	50					55					60					
aat	gat	tgc	gta	ggg	agt	gtg	gat	ttt	atc	gag	ttc	atc	aat	gga	cgt	240
Asn	Asp	Cys	Val	Gly	Ser	Val	Asp	Phe	Ile	Glu	Phe	Ile	Asn	Gly	Arg	
65					70					75				80		
tcc	agt	ttc	agt	act	gtc	ggg	cag	aag	aat	gct	aaa	ttg	aga	ttt	gca	288
Ser	Ser	Phe	Ser	Thr	Val	Gly	Gln	Lys	Asn	Ala	Lys	Leu	Arg	Phe	Ala	
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Leu	Phe	Arg	Val	Leu	Arg	Ile	Met	Val	His	Asp	Asn	Leu	Ser	Asp	Asn	
		115					120					125				
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Gln	Leu	Gln	Gln	Arg	Cys	Asp	Cys	Thr	Arg	Ser	Gly	Gly	Asp	Asn	Asp	

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 Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg
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 Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala
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 Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu
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 Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn
 115 120 125
 Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp
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 Gly Asp Gly Arg Gly Ala Lys Asn Ser Phe Glu Glu Phe Tyr Gly Arg
 145 150 155 160

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Val Pro Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln	
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atc ttg ata gat cgg ggg ttg gag acc aag gcc aaa atc ttc cct tgt	627
Ile Leu Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys	
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gag gac ttt gag cct cct gtt ata cca tcc aag aga agc cct gat aat	675
Glu Asp Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn	
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Pro Ser Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu	
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Ile Leu His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His	
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Ala Lys Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu	
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Lys Asp Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly	
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Ala Ala Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro	
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Asn Tyr Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile	
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Trp Lys Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys	
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Pro Ala Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln	
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Gly Ile Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu	
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 Glu Tyr Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His
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 Ser Leu Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro
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 Tyr Thr Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe
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 Asn Gln Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu
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 gga acc caa gac cga cga aaa cag gat gtt ggc cga cgc caa gct gcc 1539
 Gly Thr Gln Asp Arg Arg Lys Gln Asp Val Gly Arg Arg Gln Ala Ala
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 50 55 60

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 Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp Gly Arg
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 Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp Lys Phe
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 Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys Glu Asp
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 210 215 220
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 225 230 235 240
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 260 265 270
 Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu Lys Asp
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 405 410 415
 Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe Ser Ser
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 Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys Gln Cys
 435 440 445
 Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser Ile Asn
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 465 470 475 480
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 Gly Ser Ser Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly
 30 35 40 45
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 Ala Ser Thr Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile
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Thr	Thr	Ser	Thr	Arg	Ala	Arg	Arg	Tyr	Ala	Val	Ser	Ala	Lys	Phe	Pro	
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Arg	Leu	Ser	Asn	Lys	Gly	Lys	Asp	Tyr	Met	Arg	Cys	Val	Leu	Gln	Tyr	
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acc	gtc	aaa	aat	gaa	caa	aaa	gtt	gat	tgt	ggt	ggc	tca	tat	atc	aag	339
Thr	Val	Lys	Asn	Glu	Gln	Lys	Val	Asp	Cys	Gly	Gly	Ser	Tyr	Ile	Lys	
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Leu	Leu	Pro	Ser	Lys	Leu	Arg	Thr	Gly	Asp	Gly	Asp	Gly	Val	Ser	Glu	
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Tyr	Ser	Ile	Met	Phe	Gly	Pro	Asp	Ser	Thr	Gly	Ala	Ser	Arg	Thr	Val	
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Gln	Asn	Lys	Val	Glu	Thr	Asp	Gln	Leu	Thr	His	Gln	Tyr	Thr	Thr	Ser	
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Trp	Ser	Pro	Asp	Trp	Thr	Tyr	Asn	Val	Leu	Val	Asp	Asn	Lys	Glu	Ser	
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Gln	Ala	Gly	Asn	Leu	Ala	Asp	Asp	Cys	Glu	Leu	Leu	Pro	Gln	Lys	Arg	
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Ile	Phe	Arg	Pro	Ser	Cys	Arg	Lys	Gln	Ser	Lys	Pro	Val	Thr	Cys	Val	
				210					215					220		
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Asp	Val	Lys	His	His	Ala	Pro	Arg	Arg	Asn	Val	Lys	Pro	Ala	Gly	His	
			225					230					235			
gat	gac	att	cca	gcg	cga	cgg	acg	acg	ccg	gaa	gcg	gtc	cgg	aaa	ggc	771
Asp	Asp	Ile	Pro	Ala	Arg	Arg	Thr	Thr	Pro	Glu	Ala	Val	Arg	Lys	Gly	
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Arg	Thr	Asn	Glu	Arg	Pro	Asp	Arg	Thr	Trp	Ala	Thr	Gly	Thr	Thr	Pro	
	255					260					265					
cgg	cca	cgg	cgt	tac	aag	gga	gag	acg	aag	gcc	aaa	aag	cac	cca	cgg	867
Arg	Pro	Arg	Arg	Tyr	Lys	Gly	Glu	Thr	Lys	Ala	Lys	Lys	His	Pro	Arg	
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 Lys Val Ala Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly
 350 355 360 365

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 385 390 395

cgc acc ggg gag ctg gcc acc ccg gtg acg atg ctg cct gat ccg ttg 1251
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 Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile Thr Thr Ser
 50 55 60
 Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro Arg Leu Ser
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Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr	
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gag gct gag ctc caa gac atg atc aac gag gtt gat gca gat gga aac	144
Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn	
35 40 45	
ggc act atc gac ttc ccc gag ttc ctg aac ctg atg gct aag aag atg	192
Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met	
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aaa gac act gac tcc gag gaa gag cta aaa gaa gcc ttc agg gtt ttc	240
Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe	
65 70 75 80	
gac aaa gac cag aac ggt ttc atc tcc gct gct gag cta cgc cat gtg	288
Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val	
85 90 95	
atg acc aat ctt ggt gag aag cta act gat gaa gaa gtg gaa gag atg	336
Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met	
100 105 110	
atc cgt gag gct gat gtt gat gga gat ggt cag att aac tat gaa gag	384
Ile Arg Glu Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu	
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Phe Val Lys Ile Met Met Ala Lys	
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 Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met
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tctctcgttc tgtcacag c tcc cca gct cct caa gtg gca ttg tca att cct 315
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Phe Thr Phe Glu Asp Met Leu Cys Phe Gln Lys
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Asn Met Ser Leu Ser Pro Ser Phe Leu
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 160 165 170

ctc gtt gga aag ctc ttc aaa aaa act ttg aag cgt gtt gaa ctc agg 757
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 175 180 185 190

gac gaa ctt ttt gcc caa atc tcc aaa cag act aga cat aat cct gac 805
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 195 200 205

agg caa tac ttg atc aaa gct tgg gaa ttg atg tac tta tgt gcc tcc 853
 Arg Gln Tyr Leu Ile Lys Ala Trp Glu Leu Met Tyr Leu Cys Ala Ser
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 Arg His Thr Thr Pro Gly Arg Glu Glu Ile Glu Ala Leu Leu Thr Gly
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 Arg Lys Leu Thr Thr Ile Val Phe Phe Leu Asp Glu Thr Phe Glu Glu
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ctcaactgcat tgacatctgt ttcaggag cta gct gga aca att aaa cta tca 1247
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gct ttc tct agc ttt agt ttg ttt gaa tgt cgt aaa gtt gtt tca agt 1295
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 Ser Lys Ser Ser Asp Pro Gly Asn G

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125

Lys Ala Leu Pro Tyr Gly Asn Ser Val Phe Phe Ser Val Arg Lys Ile
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Gly	Asn	Arg	Asn	Asn	Asn	Asn	Lys	Asn	Ala	Gly	Gly	Val	Glu	Thr	Ser	
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Val	Asp	Val	Pro	Val	Ile	Leu	Ser	Thr	Arg	Glu	Ser	Gln	Gly	Thr	Arg	
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Cys	Glu	Trp	Phe	Ala	Thr	Pro	Thr	Asp	Pro	Gln	Arg	Pro	Gly	Val	Tyr	
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Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr	
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Ser Pro Ala Ile Asn Ala Val Lys Ser Ala Ser Asn Arg Ser Ser Ala	
245 250 255	
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Ile Gly Ser Arg Asn Ser Asp Leu Asn Asn Ala Ala Asn Asp Glu Arg	
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His Tyr Ala Arg Ser Gly Thr Tyr Gln Ile Asn Ala Val Thr Val Leu	
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Arg Val Leu Gly Arg Gly Ala Arg Arg Asp Val Lys Ser Ala Tyr His	
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Gly Thr Cys Gly Thr Gly Pro Arg Met Lys Val Ile Thr Leu Ala Val	
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Gln Glu Asn Ile Arg Asn Arg Ile Ile Leu Glu Leu Arg Thr Leu His	
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Lys Thr Ser Tyr Gln Tyr Ile Val Pro Tyr Tyr Asp Gly Ile Tyr Thr	
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Ile Met Asn Lys Thr Ala Thr Ile Arg Ala Pro Val Leu Gly Thr Met	
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Gln	His	Thr	Leu	Ser	Lys	Asp	Val	Thr	Ser	Val	Glu	Ser	Pro	Glu	Arg	
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Tyr	Pro	Gln	Gln	Leu	Pro	Gln	Ala	Ser	Gln	His	Gln	Leu	Gln	Gln	Gln	
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Gln	Gln	Lys	Arg	Pro	Ala	Leu	Gln	Pro	Lys	Gln	Glu	Gln	Pro	Glu	Val	
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Ser	Asn	His	Asp	Ile	Trp	Asn	Asn	Arg	Asn	Arg	Asp	Lys	Tyr	Ile	Ile	
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Met	Glu	Pro	Ser	Thr	Val	Ser	Lys	Glu	Phe	Arg	Ser	Ile	Ile	Ser	Glu	
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 Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile
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 Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr
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 Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr

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Arg	Lys	Pro	Pro	Ser	Asp	Gly	Phe	Leu	Lys	Leu	Pro	Ala	Ser	Ser	Ile	
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Ile	Ser	Ala	Val	Asn	Val	Ser	Ala	Gln	Ala	Ser	Leu	Thr	Ala	Asp	Phe	
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Pro	Ala	Leu	Ser	Glu	Thr	Ile	Leu	Lys	Glu	Gly	Arg	Asn	Asn	Gly	Lys	
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Glu	Lys	Ala	Glu	Asn	Ile	Val	Trp	His	Glu	Ser	Ser	Ile	Cys	Arg	Cys	
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Asp	Arg	Gln	Gln	Leu	Leu	Gln	Gln	Lys	Gly	Cys	Val	Val	Trp	Ile	Thr	
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Thr	Glu	Asn	Ile	Arg	Arg	Ile	Gly	Glu	Val	Ala	Lys	Leu	Phe	Ala	Asp	
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Val	Gly	Val	Ile	Cys	Ile	Ala	Ser	Leu	Ile	Ser	Pro	Tyr	Arg	Arg	Asp	
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Leu	Tyr	Lys	Leu	Ala	Arg	Ala	Gly	Lys	Ile	Lys	Gly	Phe	Thr	Gly	Ile	
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Asp	Asp	Pro	Tyr	Glu	Ala	Pro	Val	Asn	Cys	Glu	Val	Val	Leu	Lys	His	
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Thr	Gly	Asp	Asp	Glu	Ser	Cys	Ser	Pro	Arg	Gln	Met	Ala	Glu	Asn	Ile	

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 Leu Lys Glu Gly Arg Asn Asn Gly Lys Glu Lys Ala Glu Asn Ile Val
 85 90 95
 Trp His Glu Ser Ser Ile Cys Arg Cys Asp Arg Gln Gln Leu Leu Gln
 100 105 110
 Gln Lys Gly Cys Val Val Trp Ile Thr Gly Leu Ser Gly Ser Gly Lys
 115 120 125
 Ser Thr Val Ala Cys Ala Leu Ser Lys Ala Leu Phe Glu Arg Gly Lys
 130 135 140
 Leu Thr Tyr Thr Leu Asp Gly Asp Asn Val Arg His Gly Leu Asn Arg
 145 150 155 160
 Asp Leu Thr Phe Lys Ala Glu His Arg Thr Glu Asn Ile Arg Arg Ile
 165 170 175
 Gly Glu Val Ala Lys Leu Phe Ala Asp Val Gly Val Ile Cys Ile Ala
 180 185 190
 Ser Leu Ile Ser Pro Tyr Arg Arg Asp Arg Asp Ala Cys Arg Ser Leu
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 Leu Pro Asp Gly Asp Phe Val Glu Val Phe Met Asp Val Pro Leu His
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Val Cys Glu Ser Arg Asp Pro Lys Gly Leu Tyr Lys Leu Ala Arg Ala
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 Ala Ser Arg Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn
 95 100 105

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Leu Glu Asp Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly	145	150	155	
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Ser Leu Glu Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu	160	165	170	
tct tgg aaa ctt cgg ttg aaa gtt gct ctt ggt gct gca aag gga ctt				579
Ser Trp Lys Leu Arg Leu Lys Val Ala Leu Gly Ala Ala Lys Gly Leu	175	180	185	
gct ttt ctt cac agt tcc gag aca aga gtg ata tac cga gat ttc aag				627
Ala Phe Leu His Ser Ser Glu Thr Arg Val Ile Tyr Arg Asp Phe Lys	190	195	200	205
act tct aat atc ctt ctt gac tcg gag tac aac gca aag ctt tct gat				675
Thr Ser Asn Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp	210	215	220	
ttt ggg ttg gct aag gat ggg cca ata ggt gat aaa agt cat gtc tct				723
Phe Gly Leu Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser	225	230	235	
aca cga gtc atg ggt aca cac gga tat gca gct cct gaa tac ctt gca				771
Thr Arg Val Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala	240	245	250	
acc ggt cat cta aca aca aag agt gat gtc tat agc ttc ggg gtt gtc				819
Thr Gly His Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val	255	260	265	
ctt ctg gag ctg ttg tct ggt cgt cga gca gtg gac aag aac cgc cca				867
Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro	270	275	280	285
tct gga gag agg aac ctt gtg gag tgg gct aaa cca tac ctc gta aac				915
Ser Gly Glu Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn	290	295	300	
aaa aga aag ata ttc cga gtc att gat aat cgt ctt cag gac cag tac				963
Lys Arg Lys Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr	305	310	315	
tct atg gaa gaa gca tgt aaa gtg gct act ctg tct ctg aga tgt ctc				1011
Ser Met Glu Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu	320	325	330	
acc aca gag att aag ctg aga cca aac atg agc gag gtt gtt tcg cac				1059
Thr Thr Glu Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His	335	340	345	

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 Leu Glu His Ile Gln Ser Leu Asn Ala Ala Ile Gly Gly Asn Met Asp
 350 355 360 365

aaa aca gat aga aga atg cgt agg aga agt gac agt gtt gtc agc aaa 1155
 Lys Thr Asp Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys
 370 375 380

aaa gtg aat gca ggt ttt gct cga cag act gct gtt ggc agt aca gtt 1203
 Lys Val Asn Ala Gly Phe Ala Arg Gln Thr Ala Val Gly Ser Thr Val
 385 390 395

gtt gct tat cct cgc cca tca gcc tcg cca ctg tat gtt tga 1245
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Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu Lys Ser Ala
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Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly
 65 70 75 80

Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr Ala Ser Arg
 85 90 95

Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn Gln Asp Gly
 100 105 110

Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr Leu Gly Gln
 115 120 125

Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys Leu Glu Asp
 130 135 140

Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly Ser Leu Glu
 145 150 155 160

Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu Ser Trp Lys

165 170 175
 Leu Arg Leu Lys Val Ala Leu Gly Ala Ala Lys Gly Leu Ala Phe Leu
 180 185 190
 His Ser Ser Glu Thr Arg Val Ile Tyr Arg Asp Phe Lys Thr Ser Asn
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 Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp Phe Gly Leu
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 Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser Thr Arg Val
 225 230 235 240
 Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala Thr Gly His
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 260 265 270
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 275 280 285
 Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn Lys Arg Lys
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 305 310 315 320
 Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu Thr Thr Glu
 325 330 335
 Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His Leu Glu His
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 Ile Gln Ser Leu Asn Ala Ala Ile Gly Gly Asn Met Asp Lys Thr Asp
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 Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys Lys Val Asn
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 Met Leu Glu Lys Lys Leu Ala Ala Ala Glu Val Ser Glu Glu
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 gag caa aat aac ttg cta aag gat ttg gag atg aag gaa act gaa tat 158
 Glu Gln Asn Asn Leu Leu Lys Asp Leu Glu Met Lys Glu Thr Glu Tyr
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 atg cgc cgt cag agg cat aaa atg gga gct gat gac ttt gag cca ttg 206

Met Arg Arg Gln Arg His Lys Met Gly Ala Asp Asp Phe Glu Pro Leu
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 Thr Met Ile Gly Lys Gly Ala Phe Gly Glu
 50 55
 catagtctgt tactctgttt tctcagcctc tcattggcat gcatcatctt gaaatgttct. 316
 ctgtgatgca tccttcttga aaggctcttct taggccattt tttttaccac agctaatttt 376
 tcaaaaaagt atggcatgct aatttttctc tttctctttg cag gtt agg atc tgt 431
 Val Arg Ile Cys
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 agg gag aag gga aca ggc aat gtc tat gca atg aag aag ctt aag aaa 479
 Arg Glu Lys Gly Thr Gly Asn Val Tyr Ala Met Lys Lys Leu Lys Lys
 65 70 75
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 Ser Glu Met Leu Arg Arg Gly Gln Val
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 Val
 gaa cat gta aaa gca gag aga aat tta ctt gca gaa gtt gat agc aat 631
 Glu His Val Lys Ala Glu Arg Asn Leu Leu Ala Glu Val Asp Ser Asn
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 Cys Ile Val Lys Leu Tyr Cys Ser Phe Gln Asp Glu Glu Tyr Leu Tyr
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 ctc ata atg gag tat tta cct ggt ggg gat atg atg act tta ctt atg 727
 Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp Met Met Thr Leu Leu Met
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 Arg Lys Asp Thr Leu Thr Glu Asp Glu Ala Arg Phe Tyr Ile Gly Glu
 135 140 145 150
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 g Asp Ile Lys Pro Asp Asn Leu Leu Leu
 s 170 175
 gac aaa gac ggc cac atg aaa ttg tca gat ttt gga tta tgt aaa cca 982
 Asp Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro
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 tta gac tgt agt aat ctt caa gag aaa gac ttt aca gtt gca aga aac 1030

Leu Asp Cys Ser Asn Leu Gln Glu Lys Asp Phe Thr Val Ala Arg Asn
 195 200 205
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 Thr Gln Gln Glu Gln Leu Leu Asn Trp Gln Arg Asn Arg Arg Met Leu
 225 230 235
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 Ala Tyr Ser Thr Val Gly Thr Pro
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 Asp Tyr Ile Ala Pro Glu Val Leu Leu Lys Lys Gly Tyr Gly Met Glu
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 Cys Asp Trp
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 Met Thr Thr Cys Arg Lys
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 Ile Val Asn Trp Arg Asn Tyr Leu Lys Phe Pro Asp Glu Val
 295 300 305
 aga cta tca cca gaa gcc aag gat ctt att tgt agg ctt tta tgc aat 1773
 Arg Leu Ser Pro Glu Ala Lys Asp Leu Ile Cys Arg Leu Leu Cys Asn
 310 315 320
 gtt gaa caa agg ctt gga aca aaa gga gca gat gaa att aag 1815
 Val Glu Gln Arg Leu Gly Thr Lys Gly Ala Asp Glu Ile Lys
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Arg	Gln	Arg	His	Lys	Met	Gly	Ala	Asp	Asp	Phe	Glu	Pro	Leu	Thr	Met	
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His	Asn	Tyr	Ile	His	Arg	Asp	Ile	Lys	Pro	Asp	Asn	Leu	Leu	Leu	Asp	
				165					170					175		
Lys	Asp	Gly	His	Met	Lys	Leu	Ser	Asp	Phe	Gly	Leu	Cys	Lys	Pro	Leu	

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Ser	Gly	Ala	Leu	Gln	Ser	Asp	Gly	Arg	Pro	Val	Ala	Thr	Arg	Arg	Thr
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Gln	Gln	Glu	Gln	Leu	Leu	Asn	Trp	Gln	Arg	Asn	Arg	Arg	Met	Leu	Ala
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Tyr	Ser	Thr	Val	Gly	Thr	Pro	Asp	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Leu
				245					250					255	
Lys	Lys	Gly	Tyr	Gly	Met	Glu	Cys	Asp	Trp	Trp	Ser	Leu	Gly	Ala	Ile
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Leu	Leu	Cys	Asn	Val	Glu	Gln	Arg	Leu	Gly	Thr	Lys	Gly	Ala	Asp	Glu
				325					330					335	
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			340					345					350		
Gln	Met	Lys	Ala	Ala	Phe	Ile	Pro	Gln	Val	Asn	Asp	Glu	Leu	Asp	Thr
		355					360					365			
Gln	Asn	Phe	Glu	Lys	Phe	Glu	Glu	Thr	Asp	Lys	Gln	Val	Pro	Lys	Ser
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Phe	Val	Gly	Tyr	Thr	Tyr	Lys	Asn	Val	Glu	Ile	Val	Asn	Asp	Asp	Gln
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			420					425					430		
Pro	Ser	Ile	Lys	Ser	Leu	Phe	Glu	Asp	Glu	Thr	Ser	Gly	Gly	Thr	Thr
		435					440					445			
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Asp Arg Arg Thr Arg Trp Pro Ala Trp Lys Ala Arg Arg Asp Arg His
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Lys Arg Arg Glu Ser Cys Val Ser Leu Ala His Glu Arg Asp Tyr Ala
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Leu Thr Ala Arg Trp Asp Arg Ser Ile Ala Met Thr Asp Asp Thr Asn
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cca caa acc caa cgt aaa ttt gag aaa cat act cgg gat gta gaa gct 390
Pro Gln Thr Gln Arg Lys Phe Glu Lys His Thr Arg Asp Val Glu Ala
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Val Arg Phe Ser Pro Arg Asp Arg Leu Ile Val Ser Ala Gly Ala Asp
      125                      130                      135

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Gly Val Ile Ala Val Cys Pro Val Ala Gly Glu Cys Asp Asp Asp Asp
      140                      145                      150

gcc cgt gat ggt cat gaa gat tgt gtt agt agt att tgc ttt tca cca 534
Ala Arg Asp Gly His Glu Asp Cys Val Ser Ser Ile Cys Phe Ser Pro
      155                      160                      165

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Ala Trp Lys Ala Arg Arg Asp Arg His Ser Val Arg Ser Asp Ser Gly
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Leu Asp Ser His Ala Leu Glu Gly Gly Lys Arg Arg Glu Ser Cys Val
  65           70           75           80
Ser Leu Ala His Glu Arg Asp Tyr Ala Leu Thr Ala Arg Trp Asp Arg
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Ser Ile Ala Met Thr Asp Asp Thr Asn Pro Gln Thr Gln Arg Lys Phe
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 Cys Val Ser Ser Ile Cys Phe Ser Pro Ser Leu Glu His Pro Ile Leu
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 Phe Ser Gly Ser Cys Ile Tyr Phe Ile Lys Val Trp Asn Val Asn Gly
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 Arg Thr Gln Ser Glu Glu Gly Arg Leu Cys Ala Lys Gly Gly Lys Ser
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 sp Ser Phe Gly Tyr Thr Thr Asp Glu
 20 25

cag agt cca aga ggg tac gga agt aat tac caa tct atg ctt gaa ggt 327
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 30 35 40

tac gat gaa gat gct aca cta atc gag gaa tat tcc ggc aac cac cac 375
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 45 50 55

cac atg ggt cta tcg gag aag aag aga aga tta aaa gtt gac caa gtc 423
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 Arg Lys Thr Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val
 95 100 105

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gaa aaa gat tac ggt gtt ctt aag ggt caa tac gat tct ctc cgc cac 615
 Glu Lys Asp Tyr Gly Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His
 125 130 135

aat ttc gat tct ctc cgc cgt gac aat gat tcc ctt ctc caa gag 660
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 140 145 150

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 Ile Ser Lys Ile Lys Ala Lys Val
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aac ggt gaa gaa gat aac aac aac aac aaa gct att acg gag ggt gtt 821
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 165 170 175

aag gaa gag gaa gtt cac aag acg gat tcg att cct tcg tct cct ctg 869
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Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser Phe Thr
 195 200 205 210

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 215 220 225

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 Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser
 230 235 240

gat aac gga aga ttg acg ccg cct gtg acg gtt act ggc ggg agt ttc 1061
 Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe
 245 250 255

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agc ggt gaa gaa gct tgt ggt ttc ttc tcc gat gaa cag ccg ccg tca 1157
 Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser
 275 280 285 290

ctt cat tgg tac tct gct tca gat cat tgg act tga gaattgttta 1203
 Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr
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Ser Thr Asp Ser Phe Gly Tyr Thr Thr Asp Glu Gln Ser Pro Arg Gly
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Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly Tyr Asp Glu Asp Ala
 35 40 45

Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His His Met Gly Leu Ser
 50 55 60

Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val Lys Ala Leu Glu Lys
 65 70 75 80

Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr Lys Leu
 85 90 95

Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp Phe Gln
 100 105 110

Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly
 115 120 125
 Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His Asn Phe Asp Ser Leu
 130 135 140
 Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu Ile Ser Lys Ile Lys Ala
 145 150 155 160
 Lys Val Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu
 165 170 175
 Gly Val Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser
 180 185 190
 Pro Leu Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser
 195 200 205
 Phe Thr Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala
 210 215 220
 Gly Ser Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr
 225 230 235 240
 Ser Ser Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly
 245 250 255
 Ser Phe Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp
 260 265 270
 Phe Leu Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro
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 Pro Ser Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr
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 1 5 10
 agc tcg atc cgt tgg ttt gcc aac cga tta gtg agt ggt agc ctg tta 99
 Ser Ser Ile Arg Trp Phe Ala Asn Arg Leu Val Ser Gly Ser Leu Leu
 15 20 25
 ttg tgt gct aac gcc tac agt cgt cgt act ccc gcg tcc ggg gcc gca 147

Leu	Cys	Ala	Asn	Ala	Tyr	Ser	Arg	Arg	Thr	Pro	Ala	Ser	Gly	Ala	Ala		
			30					35					40				
tta	cag	cag	atg	aac	cgt	gcc	agt	cag	tca	gtg	aat	tac	cga	cga	cgt	195	
Leu	Gln	Gln	Met	Asn	Arg	Ala	Ser	Gln	Ser	Val	Asn	Tyr	Arg	Arg	Arg		
		45					50					55					
gag	ctg	tca	tta	atc	agc	ggc	cgg	aaa	cag	ggg	gtc	cag	tct	ctg	ggg	243	
Glu	Leu	Ser	Leu	Ile	Ser	Gly	Arg	Lys	Gln	Gly	Val	Gln	Ser	Leu	Gly		
		60				65					70						
tat	aga	ctt	gca	cgc	ctc	gat	aac	cgc	gct	ctt	gca	caa	ttg	ttg	cac	291	
Tyr	Arg	Leu	Ala	Arg	Leu	Asp	Asn	Arg	Ala	Leu	Ala	Gln	Leu	Leu	His		
		75			80					85					90		
agg	gat	ggc	cag	ccc	gag	gaa	gtg	gta	cag	cgc	ggc	aat	gaa	atc	agc	339	
Arg	Asp	Gly	Gln	Pro	Glu	Glu	Val	Val	Gln	Arg	Gly	Asn	Glu	Ile	Ser		
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tat	ttc	gaa	acg	gga	ctt	gaa	ccg	acc	acg	ctt	aga	cgt	gtg	cgc	gat	387	
Tyr	Phe	Glu	Thr	Gly	Leu	Glu	Pro	Thr	Thr	Leu	Arg	Arg	Val	Arg	Asp		
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tgt	gtt	gtt	gcc	gct	ctg	cca	acc	gtt	atc	tat	acc	gga	ttc	aaa	cgt	435	
Cys	Val	Val	Ala	Ala	Leu	Pro	Thr	Val	Ile	Tyr	Thr	Gly	Phe	Lys	Arg		
			125				130					135					
gtt	tct	cct	tac	tac	gaa	ttt	atc	tcc	gtc	ggg	cgc	acg	agg	gtt	gct	483	
Val	Ser	Pro	Tyr	Tyr	Glu	Phe	Ile	Ser	Val	Gly	Arg	Thr	Arg	Val	Ala		
		140				145					150						
gat	cgt	ctt	agc	gaa	gtc	acg	caa	gtg	gtt	ccc	cga	gat	gat	aca	cgc	531	
Asp	Arg	Leu	Ser	Glu	Val	Thr	Gln	Val	Val	Pro	Arg	Asp	Asp	Thr	Arg		
					160					165					170		
tac	gtc	tac	atc	gtg	tgg	cgg	gaa	tcc	gaa	cga	tcg	aaa	tta	gag	gcg	579	
Tyr	Val	Tyr	Ile	Val	Trp	Arg	Glu	Ser	Glu	Arg	Ser	Lys	Leu	Glu	Ala		
				175					180					185			
cgg	ggg	gat	ctc	cgt	gat	cgc	gat	ggg	gaa	acg	ctg	gaa	aag	ttt	cgc	627	
Arg	Gly	Asp	Leu	Arg	Asp	Arg	Asp	Gly	Glu	Thr	Leu	Glu	Lys	Phe	Arg		
			190					195					200				
gtg	att	gct	ttt	aac	gtc	acg	ctg	gat	atc	agc	agc	agt	atg	gag	ccg	675	
Val	Ile	Ala	Phe	Asn	Val	Thr	Leu	Asp	Ile	Ser	Ser	Ser	Met	Glu	Pro		
		205					210					215					
ctg	gcg	aag	gga	gat	ttg	ccg	ccg	ttg	ctt	gct	gtt	cct	gta	ggg	gaa	723	
Leu	Ala	Lys	Gly	Asp	Leu	Pro	Pro	Leu	Leu	Ala	Val	Pro	Val	Gly	Glu		
		220				225					230						
caa	gct	aga	ttc	agc	ttg	acg	cca	acc	tgg	ttg	cca	cag	ggg	cgt	agc	771	
Gln	Ala	Arg	Phe	Ser	Leu	Thr	Pro	Thr	Trp	Leu	Pro	Gln	Gly	Arg	Ser		
		235			240				245					250			
gat	gtt	tcc	agt	agt	cga	cgt	ggg	cta	ccg	cgg	atg	gac	aaa	gtg	cct	819	
Asp	Val	Ser	Ser	Ser	Arg	Arg	Gly	Leu	Pro	Arg	Met	Asp	Lys	Val	Pro		

	255	260	265	
atc gaa tcc cgt ctc tcg acc gac gga gta ttc agc ttc tcg gta aac				867
Ile Glu Ser Arg Leu Ser Thr Asp Gly Val Phe Ser Phe Ser Val Asn	270	275	280	
gtt aac ggc gct acg cca tcg agg tgg gat cag atg ttg cgc acc gga				915
Val Asn Gly Ala Thr Pro Ser Arg Trp Asp Gln Met Leu Arg Thr Gly	285	290	295	
cgc agg ccc gtc agt aga agc gta cgt gat gtc gcc gaa aac acc att				963
Arg Arg Pro Val Ser Arg Ser Val Arg Asp Val Ala Glu Asn Thr Ile	300	305	310	
ggc ggt gaa ctg ccg ccg cgt agc tgc tcg cga ccc gat ccg ttg acc				1011
Gly Gly Glu Leu Pro Pro Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr	315	320	325	330
gct gac cgc cga cgc tgc gct agc ctg agc ctg ccc agc ctg cca gct				1059
Ala Asp Arg Arg Arg Cys Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala	335	340	345	
cga cag ccc tcc caa acg gag aaa cgc att gtc gag aat att aag tac				1107
Arg Gln Pro Ser Gln Thr Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr	350	355	360	
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Gly Ala Ala Pro	365			

<210> 76

<211> 366

<212> PRT

<213> Arabidopsis thaliana

<400> 76

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Ser Arg Arg Thr Pro Ala Ser Gly Ala Ala Leu Gln Gln Met Asn Arg	35	40	45	
Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg Glu Leu Ser Leu Ile Ser	50	55	60	
Gly Arg Lys Gln Gly Val Gln Ser Leu Gly Tyr Arg Leu Ala Arg Leu	65	70	75	80
Asp Asn Arg Ala Leu Ala Gln Leu Leu His Arg Asp Gly Gln Pro Glu	85	90	95	
Glu Val Val Gln Arg Gly Asn Glu Ile Ser Tyr Phe Glu Thr Gly Leu	100	105	110	

Glu Pro Thr Thr Leu Arg Arg Val Arg Asp Cys Val Val Ala Ala Leu
 115 120 125
 Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg Val Ser Pro Tyr Tyr Glu
 130 135 140
 Phe Ile Ser Val Gly Arg Thr Arg Val Ala Asp Arg Leu Ser Glu Val
 145 150 155 160
 Thr Gln Val Val Pro Arg Asp Asp Thr Arg Tyr Val Tyr Ile Val Trp
 165 170 175
 Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala Arg Gly Asp Leu Arg Asp
 180 185 190
 Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg Val Ile Ala Phe Asn Val
 195 200 205
 Thr Leu Asp Ile Ser Ser Ser Met Glu Pro Leu Ala Lys Gly Asp Leu
 210 215 220
 Pro Pro Leu Leu Ala Val Pro Val Gly Glu Gln Ala Arg Phe Ser Leu
 225 230 235 240
 Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser Asp Val Ser Ser Ser Arg
 245 250 255
 Arg Gly Leu Pro Arg Met Asp Lys Val Pro Ile Glu Ser Arg Leu Ser
 260 265 270
 Thr Asp Gly Val Phe Ser Phe Ser Val Asn Val Asn Gly Ala Thr Pro
 275 280 285
 Ser Arg Trp Asp Gln Met Leu Arg Thr Gly Arg Arg Pro Val Ser Arg
 290 295 300
 Ser Val Arg Asp Val Ala Glu Asn Thr Ile Gly Gly Glu Leu Pro Pro
 305 310 315 320
 Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr Ala Asp Arg Arg Arg Cys
 325 330 335
 Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala Arg Gln Pro Ser Gln Thr
 340 345 350
 Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr Gly Ala Ala Pro
 355 360 365

<210> 77
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 <212> DNA
 <213> Arabidopsis thaliana
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162

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cctttggcag gta ttt gat ggc cac ggt ggc aca gat gca gca cac ttt 671
Val Phe Asp Gly His Gly Gly Thr Asp Ala Ala His Phe
130 135

gtt aga aag aac att ctg aga ttc att gta gag gac tcc tcc ttc cca 719
Val Arg Lys Asn Ile Leu Arg Phe Ile Val Glu Asp Ser Ser Phe Pro
140 145 150

cta tgc gta aag aaa gca att aag agt gct ttc tta aaa gct gat tat 767
Leu Cys Val Lys Lys Ala Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr
155 160 165 170

gaa ttt gca gat gat tct tct ctt gac atc tct tct ggg acc act gcg 815
Glu Phe Ala Asp Asp Ser Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala
175 180 185

ctt aca gct ttt att ttt gga cg gtaagagcat ttaaattcgt atttatgaac 868
Leu Thr Ala Phe Ile Phe Gly Ar
190

ttgggaagct atatatgtta tcacctgtat aatcatcaat acttatcagg ttgcctgtgt 928

gtataagata gagaataagg cttagtgtaa agacttatgt aacgggctgt tttaccatgt 988

ttctttgtag ttttgatgtg attttgaata gaattgctac tttctttctt tacag g 1044
g

agg ttg ata att gca aat gct ggt gat tgc cga gca gta ctg ggg aga 1092
Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu Gly Arg
195 200 205 210

aga ggt agg gca att gag ttg tcc aaa gat cac aaa cca aac tgc aca 1140
Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn Cys Thr
215 220 225

gcc gag aaa gta aga ata gaa aag tta ggt gga gtt gtg tat gac ggt 1188
Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr Asp Gly
230 235 240

tac ctc aac ggg caa cta tca gtt gca cgt gcc att gga gac tgg cac 1236
Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp Trp His
245 250 255

atg aaa ggt ccc aaa ggc tct gct tgt ccg cta agc cca gag cca gag 1284
Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu Pro Glu
260 265 270

ttg caa gag aca gac ctg agt gaa gac gac gag ttc ttg ata atg gga 1332
Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile Met Gly
275 280 285 290

tgt gat ggt ctg tgg gat gtg atg agc agc cag tgc gct gtg aca ata 1380
Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val Thr Ile
295 300 305

gct agg aag gaa ctg atg att cat aat gat cca gag aga tgc tct aga 1428
 Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys Ser Arg
 310 315 320

gag ctt gtg agg gag gcc ctt aaa cgg aat aca tgt gac aat ttg aca 1476
 Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn Leu Thr
 325 330 335

gtg att gtt gtg tgc ttc tct ccg gat cct cca cag agg ata gag atc 1524
 Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile Glu Ile
 340 345 350

cga atg cag tca cgg gtg agg cgg agc ata tct gcg gaa ggg tta aac 1572
 Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly Leu Asn
 355 360 365 370

cta ctc aaa ggc gtg ctc gat ggc tat ccg tga gcatgttatg ttgtacgtta 1625
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 375 380

ctttgtgaga ctattgccaa gtttag 1650

<210> 78

<211> 380

<212> PRT

<213> Arabidopsis thaliana

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 20 25 30

Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys Pro Pro Arg His Leu
 35 40 45

Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala Asn Ala Asp Val Asp
 50 55 60

Val Cys Asn Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu
 65 70 75 80

Pro Val Tyr Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe
 85 90 95

Met Glu Asp Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly
 100 105 110

Ala Ala Ile Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly Val Phe Asp
 115 120 125

Gly His Gly Gly Thr Asp Ala Ala His Phe Val Arg Lys Asn Ile Leu
 130 135 140

Arg Phe Ile Val Glu Asp Ser Ser Phe Pro Leu Cys Val Lys Lys Ala
 145 150 155 160
 Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr Glu Phe Ala Asp Asp Ser
 165 170 175
 Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala Leu Thr Ala Phe Ile Phe
 180 185 190
 Gly Arg Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu
 195 200 205
 Gly Arg Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn
 210 215 220
 Cys Thr Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr
 225 230 235 240
 Asp Gly Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp
 245 250 255
 Trp His Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu
 260 265 270
 Pro Glu Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile
 275 280 285
 Met Gly Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val
 290 295 300
 Thr Ile Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys
 305 310 315 320
 Ser Arg Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn
 325 330 335
 Leu Thr Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile
 340 345 350
 Glu Ile Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly
 355 360 365
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 370 375 380

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 <212> DNA
 <213> Arabidopsis thaliana

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 <222> (18)..(575)

<400> 79

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gag gtg cca aag gta gca aca gag gaa tca tcg gca gag gtt aca gat      98
Glu Val Pro Lys Val Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp
                  15                      20                      25

cgt gga ttg ttc gat ttc ttg gga aag aag aaa gac gaa aca aaa cca      146
Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro
                  30                      35                      40

gag gag act ccg atc gct tca gag ttt gag cag aag gtt cat att tca      194
Glu Glu Thr Pro Ile Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser
                  45                      50                      55

gag ccg gag cca gag gtt aaa cac gaa agt ctt ctt gaa aag ctt cac      242
Glu Pro Glu Pro Glu Val Lys His Glu Ser Leu Leu Glu Lys Leu His
                  60                      65                      70                      75

cga agc gac agt tct tct agc tcc tca agt gag gaa gaa ggt tca gat      290
Arg Ser Asp Ser Ser Ser Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp
                  80                      85                      90

ggt gag aag agg aag aag aag aag gag aag aag aag cca act act gaa      338
Gly Glu Lys Arg Lys Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu
                  95                      100                      105

gtt gag gta aag gag gaa gag aag aaa ggg ttt atg gag aag ttg aaa      386
Val Glu Val Lys Glu Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys
                  110                      115                      120

gag aag ctt cct gga cac aag aaa cct gaa gac ggt tca gcc gtc gct      434
Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala
                  125                      130                      135

gcg gca ccg gtg gtt gtt cct cct cct gtg gaa gaa gcg cat cca gtg      482
Ala Ala Pro Val Val Val Pro Pro Pro Val Glu Glu Ala His Pro Val
                  140                      145                      150                      155

gag aag aaa ggg att ctt gag aag att aag gag aag ctt cca gga tac      530
Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr
                  160                      165                      170

cac cct aag acc acc gta gag gag gag aag aaa gat aaa gaa taa      575
His Pro Lys Thr Thr Val Glu Glu Glu Lys Lys Asp Lys Glu
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<210> 80

<211> 185

<212> PRT

<213> Arabidopsis thaliana

<400> 80

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 Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro Glu Glu Thr Pro Ile
 35 40 45
 Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser Glu Pro Glu Pro Glu
 50 55 60
 Val Lys His Glu Ser Leu Leu Glu Lys Leu His Arg Ser Asp Ser Ser
 65 70 75 80
 Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp Gly Glu Lys Arg Lys
 85 90 95
 Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu Val Glu Val Lys Glu
 100 105 110
 Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys Glu Lys Leu Pro Gly
 115 120 125
 His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala Ala Ala Pro Val Val
 130 135 140
 Val Pro Pro Pro Val Glu Glu Ala His Pro Val Glu Lys Lys Gly Ile
 145 150 155 160
 Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr His Pro Lys Thr Thr
 165 170 175
 Val Glu Glu Glu Lys Lys Asp Lys Glu
 180 185

<210> 81
 <211> 1376
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (20)..(1366)

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 gag gtt gcg gcg agg cta gcg gct gag gac ttg cat gac att aac aaa 100
 Glu Val Ala Ala Arg Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys
 15 20 25
 tcc ggt ggt gct gat gtc aca atg tat aag gtg acg gag aga aca act 148

Ser	Gly	Gly	Ala	Asp	Val	Thr	Met	Tyr	Lys	Val	Thr	Glu	Arg	Thr	Thr		
		30					35					40					
gaa	cat	cca	ccg	gag	caa	gat	agg	ccc	ggg	gtg	ata	ggg	tca	gtg	ttc	196	
Glu	His	Pro	Pro	Glu	Gln	Asp	Arg	Pro	Gly	Val	Ile	Gly	Ser	Val	Phe		
	45					50				55							
agg	gct	gtc	caa	gga	acg	tat	gag	cat	gcg	aga	gac	gct	gta	gtt	gga	244	
Arg	Ala	Val	Gln	Gly	Thr	Tyr	Glu	His	Ala	Arg	Asp	Ala	Val	Val	Gly		
	60				65				70						75		
aaa	acc	cac	gaa	gcg	gct	gag	tct	acc	aaa	gaa	gga	gct	cag	ata	gct	292	
Lys	Thr	His	Glu	Ala	Ala	Glu	Ser	Thr	Lys	Glu	Gly	Ala	Gln	Ile	Ala		
			80						85					90			
tca	gag	aaa	gcg	gtt	gga	gca	aag	gac	gca	acc	gtc	gag	aaa	gct	aag	340	
Ser	Glu	Lys	Ala	Val	Gly	Ala	Lys	Asp	Ala	Thr	Val	Glu	Lys	Ala	Lys		
			95					100					105				
gaa	acc	gct	gat	tat	act	gcg	gag	aag	gtg	ggg	gag	tat	aaa	gac	tat	388	
Glu	Thr	Ala	Asp	Tyr	Thr	Ala	Glu	Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr		
	110					115						120					
acg	gtt	gat	aaa	gct	aaa	gag	gct	aag	gac	aca	act	gca	gag	aag	gcg	436	
Thr	Val	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Thr	Thr	Ala	Glu	Lys	Ala		
	125					130					135						
aag	gag	act	gct	aat	tat	act	gcg	gat	aag	gcg	gtg	gaa	gca	aag	gat	484	
Lys	Glu	Thr	Ala	Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Val	Glu	Ala	Lys	Asp		
	140				145					150					155		
aag	acg	gcg	gag	aag	att	ggg	gag	tac	aaa	gac	tat	gcg	gtg	gat	aag	532	
Lys	Thr	Ala	Glu	Lys	Ile	Gly	Glu	Tyr	Lys	Asp	Tyr	Ala	Val	Asp	Lys		
				160					165					170			
gca	gta	gaa	gct	aaa	gat	aag	aca	gcg	gag	aag	gcg	aag	gag	act	tcg	580	
Ala	Val	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu	Lys	Ala	Lys	Glu	Thr	Ser		
			175					180					185				
aat	tat	acg	gcg	gat	aag	gct	aaa	gag	gct	aag	gac	aag	acg	gct	gag	628	
Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu		
	190					195						200					
aag	gtt	ggg	gag	tat	aag	gat	tac	acg	gtg	gac	aag	gcc	gtg	gaa	gct	676	
Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Asp	Lys	Ala	Val	Glu	Ala		
	205					210					215						
agg	gat	tac	aca	gcg	gag	aag	gct	att	gaa	gca	aag	gat	aag	aca	gct	724	
Arg	Asp	Tyr	Thr	Ala	Glu	Lys	Ala	Ile	Glu	Ala	Lys	Asp	Lys	Thr	Ala		
	220				225					230					235		
gag	aag	act	gga	gag	tat	aag	gac	tat	acg	gtg	gag	aag	gcg	acg	gag	772	
Glu	Lys	Thr	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Glu	Lys	Ala	Thr	Glu		
				240					245					250			
ggg	aaa	gat	gtt	acg	gtg	agt	aag	cta	gga	gag	ctg	aag	gat	agt	gcc	820	
Gly	Lys	Asp	Val	Thr	Val	Ser	Lys	Leu	Gly	Glu	Leu	Lys	Asp	Ser	Ala		

255	260	265	
gtt gag aca gcg aag aga gct atg ggt ttc ttg tcg ggg aag aca gag Val Glu Thr Ala Lys Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu 270 275 280			868
gag gcc aaa gga aaa gct gtg gag acc aaa gat act gcc aag gaa aac Glu Ala Lys Gly Lys Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn 285 290 295			916
atg gag aaa gct gga gaa gta aca aga caa aag atg gag gaa atg aga Met Glu Lys Ala Gly Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg 300 305 310 315			964
ttg gaa ggt aaa gag ctc aaa gaa gaa gct gga gca aaa gcc caa gag Leu Glu Gly Lys Glu Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu 320 325 330			1012
gca tct caa aag act agg gag agt act gag tcg gga gct caa aaa gcc Ala Ser Gln Lys Thr Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala 335 340 345			1060
gaa gag acc aaa gat tct cct gcc gtg agg gga aat gaa gcg aaa ggg Glu Glu Thr Lys Asp Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly 350 355 360			1108
act att ttt ggt gca tta ggg aat gta acg gaa gca ata aag agc aaa Thr Ile Phe Gly Ala Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys 365 370 375			1156
ctg aca atg cca tca gac att gtg gag gaa aca cgc gcg gca cgt gag Leu Thr Met Pro Ser Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu 380 385 390 395			1204
cat gga ggg acg ggt agg act gtg gtt gaa gtc aag gtc gag gat tca His Gly Gly Thr Gly Arg Thr Val Val Glu Val Lys Val Glu Asp Ser 400 405 410			1252
aag ccg ggt aag gtg gcg act tca ctg aag gcg tcg gat caa atg acc Lys Pro Gly Lys Val Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr 415 420 425			1300
ggt caa aca ttc aac gac gtt gga cgg atg gat gat gat gct cgg aaa Gly Gln Thr Phe Asn Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys 430 435 440			1348
gat aag gga aag ctg tga gaatactaga Asp Lys Gly Lys Leu 445			1376

<210> 82

<211> 448

<212> PRT

<213> Arabidopsis thaliana

<400> 82

Met Ala Ser Asp Lys Gln Lys Ala Glu Arg Ala Glu Val Ala Ala Arg
 1 5 10 15
 Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys Ser Gly Gly Ala Asp
 20 25 30
 Val Thr Met Tyr Lys Val Thr Glu Arg Thr Thr Glu His Pro Pro Glu
 35 40 45
 Gln Asp Arg Pro Gly Val Ile Gly Ser Val Phe Arg Ala Val Gln Gly
 50 55 60
 Thr Tyr Glu His Ala Arg Asp Ala Val Val Gly Lys Thr His Glu Ala
 65 70 75 80
 Ala Glu Ser Thr Lys Glu Gly Ala Gln Ile Ala Ser Glu Lys Ala Val
 85 90 95
 Gly Ala Lys Asp Ala Thr Val Glu Lys Ala Lys Glu Thr Ala Asp Tyr
 100 105 110
 Thr Ala Glu Lys Val Gly Glu Tyr Lys Asp Tyr Thr Val Asp Lys Ala
 115 120 125
 Lys Glu Ala Lys Asp Thr Thr Ala Glu Lys Ala Lys Glu Thr Ala Asn
 130 135 140
 Tyr Thr Ala Asp Lys Ala Val Glu Ala Lys Asp Lys Thr Ala Glu Lys
 145 150 155 160
 Ile Gly Glu Tyr Lys Asp Tyr Ala Val Asp Lys Ala Val Glu Ala Lys
 165 170 175
 Asp Lys Thr Ala Glu Lys Ala Lys Glu Thr Ser Asn Tyr Thr Ala Asp
 180 185 190
 Lys Ala Lys Glu Ala Lys Asp Lys Thr Ala Glu Lys Val Gly Glu Tyr
 195 200 205
 Lys Asp Tyr Thr Val Asp Lys Ala Val Glu Ala Arg Asp Tyr Thr Ala
 210 215 220
 Glu Lys Ala Ile Glu Ala Lys Asp Lys Thr Ala Glu Lys Thr Gly Glu
 225 230 235 240
 Tyr Lys Asp Tyr Thr Val Glu Lys Ala Thr Glu Gly Lys Asp Val Thr
 245 250 255
 Val Ser Lys Leu Gly Glu Leu Lys Asp Ser Ala Val Glu Thr Ala Lys
 260 265 270
 Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu Glu Ala Lys Gly Lys
 275 280 285
 Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn Met Glu Lys Ala Gly
 290 295 300

Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg Leu Glu Gly Lys Glu
 305 310 315 320
 Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu Ala Ser Gln Lys Thr
 325 330 335
 Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala Glu Glu Thr Lys Asp
 340 345 350
 Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly Thr Ile Phe Gly Ala
 355 360 365
 Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys Leu Thr Met Pro Ser
 370 375 380
 Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu His Gly Gly Thr Gly
 385 390 395 400
 Arg Thr Val Val Glu Val Lys Val Glu Asp Ser Lys Pro Gly Lys Val
 405 410 415
 Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr Gly Gln Thr Phe Asn
 420 425 430
 Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys Asp Lys Gly Lys Leu
 435 440 445

<210> 83
 <211> 561
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (18)..(548)

<400> 83
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 Met Asn Glu Met Ser Phe Phe Gly Tyr Ser Phe
 1 5 10
 atc gta gta gca tta ttc ttc gat tta act caa gcc tat cgt cac act 98
 Ile Val Val Ala Leu Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr
 15 20 25
 ccc gct caa ccg cca aaa gca aac gca aac ggt gat gtc aaa ccg caa 146
 Pro Ala Gln Pro Pro Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln
 30 35 40
 gaa acg ctc gtg gtt cac aac aag gcc cga gcc atg gtc gga gtc gga 194
 Glu Thr Leu Val Val His Asn Lys Ala Arg Ala Met Val Gly Val Gly
 45 50 55
 cca atg gtg tgg aac gaa act ctt gcg acc tat gca cag agc tac gca 242
 Pro Met Val Trp Asn Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala

60	65	70	75	
cat gaa cga gcc aga gac tgt gcc atg aag cat tcc ttg gga cca ttc				290
His Glu Arg Ala Arg Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe	80	85	90	
ggc gag aat cta gcc gcg ggt tgg gga acg atg agc ggt ccg gta gca				338
Gly Glu Asn Leu Ala Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala	95	100	105	
act gag tat tgg atg acg gag aag gaa aat tac gat tat gat agt aac				386
Thr Glu Tyr Trp Met Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn	110	115	120	
acg tgt ggt ggt gat ggt gtg tgt gga cac tac act cag atc gtg tgg				434
Thr Cys Gly Gly Asp Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp	125	130	135	
cgt gac tcg gtt cga ctt ggt tgt gcc tcc gtg aga tgt aag aat gat				482
Arg Asp Ser Val Arg Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp	140	145	150	155
gag tat att tgg gtg att tgt agc tat gat cct ccg ggg aat tac atc				530
Glu Tyr Ile Trp Val Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile	160	165	170	
ggc caa cgt cca tat tag tgattggatt tta				561
Gly Gln Arg Pro Tyr	175			

<210> 84

<211> 176

<212> PRT

<213> Arabidopsis thaliana

<400> 84

Met Asn Glu Met Ser Phe Phe Gly Tyr Ser Phe Ile Val Val Ala Leu	1	5	10	15
Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr Pro Ala Gln Pro Pro	20	25	30	
Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln Glu Thr Leu Val Val	35	40	45	
His Asn Lys Ala Arg Ala Met Val Gly Val Gly Pro Met Val Trp Asn	50	55	60	
Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala His Glu Arg Ala Arg	65	70	75	80
Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe Gly Glu Asn Leu Ala	85	90	95	
Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala Thr Glu Tyr Trp Met	100	105	110	

Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn Thr Cys Gly Gly Asp
 115 120 125
 Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp Arg Asp Ser Val Arg
 130 135 140
 Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp Glu Tyr Ile Trp Val
 145 150 155 160
 Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile Gly Gln Arg Pro Tyr
 165 170 175

<210> 85
 <211> 988
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (12)..(977)

<400> 85
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 Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe
 1 5 10
 tta gtt ttg ttg ttt gct caa gcc aat tgc caa ggt ttg aaa gta ggt 98
 Leu Val Leu Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly
 15 20 25
 ttc tac agc aaa aca tgc cca caa ctc gag ggt ata gtt aaa aag gtc 146
 Phe Tyr Ser Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val
 30 35 40 45
 gtg ttc gat gcg atg aac aaa gca cca aca ctt ggt gct cct ttg ctt 194
 Val Phe Asp Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu
 50 55 60
 aga atg ttc ttc cac gac tgc ttc gtt cgg gga tgt gac gga tca gtt 242
 Arg Met Phe Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val
 65 70 75
 ttg tta gat aaa cca aac aat caa ggt gag aag agt gca gtt cct aac 290
 Leu Leu Asp Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn
 80 85 90
 cta agt ctt cga ggg ttt ggc atc ata gac gat tcc aag gcg gct cta 338
 Leu Ser Leu Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu
 95 100 105
 gaa aaa gtg tgt ccg gga att gtt tct tgc tct gat atc ttg gca ctt 386
 Glu Lys Val Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu
 110 115 120 125

gtc gct aga gac gca atg gtt gca ctt gaa gga cca tca tgg gaa gtt 434
 Val Ala Arg Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val
 130 135 140

gaa acg gga aga aga gac ggt agg gtt tct aac atc aac gaa gtc aac 482
 Glu Thr Gly Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn
 145 150 155

ttg cca tca cct ttt gat aac atc acc aag ctt atc agc gat ttt cgc 530
 Leu Pro Ser Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg
 160 165 170

tca aag ggc ctc aac gag aag gat cta gtc att ctc tcg ggt ggt cac 578
 Ser Lys Gly Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His
 175 180 185

aca att gga atg gga cat tgt cct tta ttg aca aac cgg ctt tac aac 626
 Thr Ile Gly Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn
 190 195 200 205

ttc acc gga aaa gga gac agc gac cca agt ttg gac tcg gag tac gcc 674
 Phe Thr Gly Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala
 210 215 220

gct aag ctc agg aag aaa tgc aag ccc acc gat acg acg acg gct cta 722
 Ala Lys Leu Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu
 225 230 235

gag atg gat ccg ggg agt ttc aaa aca ttt gac ttg agc tac ttc acg 770
 Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr
 240 245 250

cta gtg gct aag aga aga gga ctt ttc cag tcg gat gct gct cta ctc 818
 Leu Val Ala Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu
 255 260 265

gac aac tcc aag act agg gct tat gtc ttg caa cag ata aga act cat 866
 Asp Asn Ser Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His
 270 275 280 285

ggg tca atg ttc ttt aac gac ttt ggt gtc tct atg gtg aaa atg ggt 914
 Gly Ser Met Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly
 290 295 300

cgg act gga gtt ctt acg ggt aag gcc ggg gag atc cgt aag acg tgt 962
 Arg Thr Gly Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys
 305 310 315

cgg tct gct aat taa gagatataga aa 989
 Arg Ser Ala Asn
 320

<210> 86
 <211> 321
 <212> PRT
 <213> Arabidopsis thaliana

<400> 86

Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe Leu Val Leu
 1 5 10 15
 Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly Phe Tyr Ser
 20 25 30
 Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val Val Phe Asp
 35 40 45
 Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu Arg Met Phe
 50 55 60
 Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp
 65 70 75 80
 Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn Leu Ser Leu
 85 90 95
 Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu Glu Lys Val
 100 105 110
 Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu Val Ala Arg
 115 120 125
 Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val Glu Thr Gly
 130 135 140
 Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn Leu Pro Ser
 145 150 155 160
 Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg Ser Lys Gly
 165 170 175
 Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His Thr Ile Gly
 180 185 190
 Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn Phe Thr Gly
 195 200 205
 Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala Ala Lys Leu
 210 215 220
 Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu Glu Met Asp
 225 230 235 240
 Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr Leu Val Ala
 245 250 255
 Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu Asp Asn Ser
 260 265 270
 Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His Gly Ser Met
 275 280 285
 Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly Arg Thr Gly

125

290 295 300

Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys Arg Ser Ala
 305 310 315 320

Asn

<210> 87
 <211> 650
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (8) .. (634)

<400> 87

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 Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu
 1 5 10

tcg ttc tcc tcc caa gtt tct caa aga cct aac acc att tcc ttc ccc 97
 Ser Phe Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro
 15 20 25 30

cgc gcg aat tca gta ttc gca tta ccg gcg aaa tcc gca cgc cgc gct 145
 Arg Ala Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala
 35 40 45

tct cta tct atc acc gcc acg gta tct gct cca ccg gag gag gag gag 193
 Ser Leu Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu
 50 55 60

ata gtt gaa ctg aag aaa tac gtc aaa tcg agg ctt ccc gga gga ttt 241
 Ile Val Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe
 65 70 75

gct gct cag aag att att ggc act gga cga cgt aag tgc gca atc gct 289
 Ala Ala Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala
 80 85 90

aga gtt gtt ctt cag gaa ggt act ggg aag gtt atc atc aac tat cgt 337
 Arg Val Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg
 95 100 105 110

gat gcc aag gag tac ctt cag gga aat cca ttg tgg ctt cag tat gtt 385
 Asp Ala Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val
 115 120 125

aaa gta cca ttg gtg act tta gga tat gag aat agc tac gac ata ttt 433
 Lys Val Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe
 130 135 140

gtg aaa gcc cat gga ggc ggt ctc tca ggt caa gct caa gca att acc 481
 Val Lys Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr

145	150	155	
ttg gga gtc gca cgt gca ctc ctg aag gta agt gca gac cac aga tcg			529
Leu Gly Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser			
160	165	170	
cct ttg aag aag gaa ggt ttg ctc act aga gat gcg aga gtg gtt gaa			577
Pro Leu Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu			
175	180	185	190
aga aag aag gcc ggg ctc aag aag gcg cgt aaa gcc cca caa ttc tcc			625
Arg Lys Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser			
	195	200	205
aag cgt taa gagttttata tatcat			650
Lys Arg			

<210> 88
 <211> 208
 <212> PRT
 <213> Arabidopsis thaliana

<400> 88
 Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu Ser Phe
 1 5 10 15
 Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro Arg Ala
 20 25 30
 Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala Ser Leu
 35 40 45
 Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu Ile Val
 50 55 60
 Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe Ala Ala
 65 70 75 80
 Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala Arg Val
 85 90 95
 Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg Asp Ala
 100 105 110
 Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val Lys Val
 115 120 125
 Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe Val Lys
 130 135 140
 Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr Leu Gly
 145 150 155 160
 Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser Pro Leu
 165 170 175

Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu Arg Lys
 180 185 190

Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser Lys Arg
 195 200 205

<210> 89

<211> 1223

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (16)..(1215)

<400> 89

aacaagtga gcaca atg ggg atc atc gaa agg att aaa gaa atc gag gcc 51
 Met Gly Ile Ile Glu Arg Ile Lys Glu Ile Glu Ala
 1 5 10

gag atg gct cgg act cag aag aat aaa gct aca gag tat cat ctt ggt 99
 Glu Met Ala Arg Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly
 15 20 25

cag ctc aag gca aag att gca aaa ctc agg aca caa ctg ttg gag cct 147
 Gln Leu Lys Ala Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro
 30 35 40

cca aaa ggt gct agt gga ggc ggg gaa ggt ttt gaa gtt acc aag tat 195
 Pro Lys Gly Ala Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr
 45 50 55 60

ggt cat gga cgt gtt gca ctt ata gga ttt cct agt gtc gga aag tcc 243
 Gly His Gly Arg Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser
 65 70 75

acg ctt ttg act atg tta act gga aca cat tct gaa gca gcc tca tat 291
 Thr Leu Leu Thr Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr
 80 85 90

gaa ttt aca aca ctt aca tgc atc cct ggt gta att cac tac aac gac 339
 Glu Phe Thr Thr Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp
 95 100 105

aca aag att cag ctt ctc gat ctt cct ggg att att gaa ggt gct tcg 387
 Thr Lys Ile Gln Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser
 110 115 120

gaa gga aag ggg cga gga agg cag gtt att gct gtt gca aag tct tcc 435
 Glu Gly Lys Gly Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser
 125 130 135 140

gac ctt gta ttg atg gtt ctt gat gcc tca aaa agc gaa ggc cac agg 483
 Asp Leu Val Leu Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg
 145 150 155

caa ata ttg act aag gaa ctt gag gca gtg ggc ttg cga cta aac aaa	531
Gln Ile Leu Thr Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys	
160 165 170	
act cct ccg cag ata tac ttt aaa aag aaa aag act ggt gga atc tct	579
Thr Pro Pro Gln Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser	
175 180 185	
ttc aac act aca gca ccc ttg act cac att gat gag aag ctc tgt tat	627
Phe Asn Thr Thr Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr	
190 195 200	
caa atc ctg cat gaa tac aag att cac aat gct gag gtg cta ttt cgt	675
Gln Ile Leu His Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg	
205 210 215 220	
gag aat gcc aca gtg gat gac ttt att gat gtc att gaa ggc aac cgc	723
Glu Asn Ala Thr Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg	
225 230 235	
aag tat att aag tgt gtt tat gtc tac atc aaa ata gat gtt gtt gga	771
Lys Tyr Ile Lys Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly	
240 245 250	
att gat gat gtg gat aga cta tcc cgg cag cca aat tcc att gtt att	819
Ile Asp Asp Val Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile	
255 260 265	
agc tgc aat ctt aag ctt aac tta gac aga cta ctt gct agg atg tgg	867
Ser Cys Asn Leu Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp	
270 275 280	
gac gaa atg ggc ctt gtg aga gtt tac tcg aag ccg caa ggc cag caa	915
Asp Glu Met Gly Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln	
285 290 295 300	
cca gat ttc gat gag cct ttt gtc ctc tca tct gat cga ggt ggc tgc	963
Pro Asp Phe Asp Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys	
305 310 315	
aca gtg gaa gac ttc tgt aac cac gtc cac agg act ctg gtg aag gat	1011
Thr Val Glu Asp Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp	
320 325 330	
atg aag tat gca ctc gtt tgg ggc aca agc aca agg cac aat cca cag	1059
Met Lys Tyr Ala Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln	
335 340 345	
aat tgt ggt ctt tct caa cat ctt gaa gac gaa gat gtt gtt cag atc	1107
Asn Cys Gly Leu Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile	
350 355 360	
gtc aag aaa aag gag aga gac gaa gga gga aga ggc cgg ttc aag tca	1155
Val Lys Lys Lys Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser	
365 370 375 380	

cac tca aac gcc cct gct aga att gca gac aga gag aaa aaa gct cct 1203
 His Ser Asn Ala Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro
 385 390 395

ctt aag caa taa gcttttag 1223
 Leu Lys Gln
 400

<210> 90
 <211> 399
 <212> PRT
 <213> Arabidopsis thaliana

<400> 90
 Met Gly Ile Ile Glu Arg Ile Lys Glu Ile Glu Ala Glu Met Ala Arg
 1 5 10 15
 Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly Gln Leu Lys Ala
 20 25 30
 Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro Pro Lys Gly Ala
 35 40 45
 Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr Gly His Gly Arg
 50 55 60
 Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Thr
 65 70 75 80
 Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr Glu Phe Thr Thr
 85 90 95
 Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp Thr Lys Ile Gln
 100 105 110
 Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly
 115 120 125
 Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser Asp Leu Val Leu
 130 135 140
 Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg Gln Ile Leu Thr
 145 150 155 160
 Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys Thr Pro Pro Gln
 165 170 175
 Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser Phe Asn Thr Thr
 180 185 190
 Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr Gln Ile Leu His
 195 200 205
 Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg Glu Asn Ala Thr
 210 215 220

Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg Lys Tyr Ile Lys
 225 230 235 240
 Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly Ile Asp Asp Val
 245 250 255
 Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile Ser Cys Asn Leu
 260 265 270
 Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp Asp Glu Met Gly
 275 280 285
 Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln Pro Asp Phe Asp
 290 295 300
 Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys Thr Val Glu Asp
 305 310 315 320
 Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp Met Lys Tyr Ala
 325 330 335
 Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln Asn Cys Gly Leu
 340 345 350
 Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile Val Lys Lys Lys
 355 360 365
 Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser His Ser Asn Ala
 370 375 380
 Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro Leu Lys Gln
 385 390 395

<210> 91
 <211> 536
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (12)..(524)

<400> 91
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 Met Thr Ser Ser Asp Gln Ser Pro Ser His Asp Val Phe
 1 5 10
 gtc tac ggc agt ttc caa gaa cca gcc gtt gtt aat tta att ctc gaa 98
 Val Tyr Gly Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu
 15 20 25
 tgt gct ccg gtc atg gtt tcc gct caa ctc cac ggc tat cac ttg tat 146
 Cys Ala Pro Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr
 30 35 40 45

aga ctt aaa ggt cgt ttg cat cca tgt att tct cct tcc gac aat gga 194
 Arg Leu Lys Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly
 50 55 60

tta atc aat ggc aag ata cta act gga tta aca gat tct cag tta gag 242
 Leu Ile Asn Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu
 65 70 75

agt tta gat atg att gaa gga act gaa tat gtg agg aag act gtt gaa 290
 Ser Leu Asp Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu
 80 85 90

gtt gtt ttg act gat act ttg gag aag aag caa gtt gaa aca att gta 338
 Val Val Leu Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val
 95 100 105

tgg gca aac aag gat gat cct aat atg tat gga gaa tgg gat ttc gag 386
 Trp Ala Asn Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu
 110 115 120 125

gaa tgg aag agg ctt cat atg gag aaa ttt ata gag gcg gcg acg aaa 434
 Glu Trp Lys Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys
 130 135 140

ttc atg gag tgg aag aag aat ccg aat ggg aga agt agg gaa gag ttt 482
 Phe Met Glu Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe
 145 150 155

gag aag ttt gta caa gat gat tct tct ccg gct tcg gct tga 524
 Glu Lys Phe Val Gln Asp Asp Ser Ser Pro Ala Ser Ala
 160 165 170

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<211> 170

<212> PRT

<213> Arabidopsis thaliana

<400> 92

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Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu Cys Ala Pro
 20 25 30

Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr Arg Leu Lys
 35 40 45

Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly Leu Ile Asn
 50 55 60

Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu Ser Leu Asp
 65 70 75 80

Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu Val Val Leu

	85		90		95
Thr Asp Thr	Leu Glu Lys Lys Gln Val Glu Thr Ile Val Trp Ala Asn				
	100		105		110
Lys Asp Asp	Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu Glu Trp Lys				
	115		120		125
Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys Phe Met Glu					
	130		135		140
Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe Glu Lys Phe					
	145		150		155
Val Gln Asp Asp Ser Ser Pro Ala Ser Ala					
	165		170		

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 <222> (16)..(71)

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 1 5 10

aaa tgt ggt gat tcg tgc ag gtaaacccta gattctctct tcattaactt 101
 Lys Cys Gly Asp Ser Cys Se
 15

atcatgcata tatatcctaa tatacatgtg gttacatatt ccttaagata aattttgaaa 161

tcttataactt ctgttggtttt tttgggtatga caaag t tgc gag aag aac tac aac 215
 r Cys Glu Lys Asn Tyr Asn
 20 25

aag gag tgt gat aac tgt agc tgt gga tca aac tgc agc tgc ggg tca 263
 Lys Glu Cys Asp Asn Cys Ser Cys Gly Ser Asn Cys Ser Cys Gly Ser
 30 35 40

agc tgt aac tgt tga agaaattatc agcat 293
 Ser Cys Asn Cys
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<210> 94

<211> 45
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 <213> Arabidopsis thaliana

<400> 94
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 20 25 30
 Cys Gly Ser Asn Cys Ser Cys Gly Ser Ser Cys Asn Cys
 35 40 45

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 <222> (14)..(868)

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 1 5 10
 cgc ctc aga tct ctc gct ctt tcg tct tct ttt tct tct ttc cga ttt 97
 Arg Leu Arg Ser Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe
 15 20 25
 gcc cat cgt cct ctg tca tcg att tca ccg aga aag tta ccg aat ttt 145
 Ala His Arg Pro Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe
 30 35 40
 cgt gct ttc tct ggt acc gct atg aca gat act aaa gat gct ggt atg 193
 Arg Ala Phe Ser Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met
 45 50 55 60
 gat gct gtt cag aga cgt ctc atg ttt gag gat gaa tgc att ctt gtt 241
 Asp Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val
 65 70 75
 gat gaa act gat cgt gtt gtg ggg cat gac agc aag tat aat tgt cat 289
 Asp Glu Thr Asp Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His
 80 85 90
 ctg atg gaa aat att gaa gcc aag aat ttg ctg cac agg gct ttt agt 337
 Leu Met Glu Asn Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser
 95 100 105
 gta ttt tta ttc aac tcg aag tat gag ttg ctt ctc cag caa agg tca 385
 Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser
 110 115 120

aac aca aag gtt acg ttc cct cta gtg tgg act aac act tgt tgc agc 433
 Asn Thr Lys Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser
 125 130 135 140

cat cct ctt tac cgt gaa tca gag ctt atc cag gac aat gca cta ggt 481
 His Pro Leu Tyr Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly
 145 150 155

gtg agg aat gct gca caa aga aag ctt ctc gat gag ctt ggt att gta 529
 Val Arg Asn Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val
 160 165 170

gct gaa gat gta cca gtc gat gag ttc act ccc ttg gga cgt atg ctg 577
 Ala Glu Asp Val Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu
 175 180 185

tac aag gct cct tct gat ggc aaa tgg gga gag cat gaa ctt gat tac 625
 Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr
 190 195 200

ttg ctc ttc atc gtg cga gac gtg aag gtt caa cca aac cca gat gaa 673
 Leu Leu Phe Ile Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu
 205 210 215 220

gta gct gag atc aag tat gtg agc cgg gaa gag ctg aag gag ctg gtg 721
 Val Ala Glu Ile Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val
 225 230 235

aag aaa gca gat gca ggt gag gaa ggt ttg aaa ctg tca cca tgg ttc 769
 Lys Lys Ala Asp Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe
 240 245 250

aga ttg gtg gtg gac aat ttc ttg atg aag tgg tgg gat cat gta gag 817
 Arg Leu Val Val Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu
 255 260 265

aaa gga act ttg gtt gaa gct ata gac atg aaa acc atc cac aaa ctc 865
 Lys Gly Thr Leu Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
 270 275 280

tga acatcttttt tt 880
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<210> 96

<211> 284

<212> PRT

<213> Arabidopsis thaliana

<400> 96

Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile Arg Leu Arg Ser
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Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe Ala His Arg Pro
 20 25 30

Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe Arg Ala Phe Ser
 35 40 45
 Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met Asp Ala Val Gln
 50 55 60
 Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val Asp Glu Thr Asp
 65 70 75 80
 Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Asn
 85 90 95
 Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe
 100 105 110
 Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Asn Thr Lys Val
 115 120 125
 Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr
 130 135 140
 Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly Val Arg Asn Ala
 145 150 155 160
 Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val Ala Glu Asp Val
 165 170 175
 Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro
 180 185 190
 Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile
 195 200 205
 Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu Val Ala Glu Ile
 210 215 220
 Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val Lys Lys Ala Asp
 225 230 235 240
 Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val
 245 250 255
 Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu Lys Gly Thr Leu
 260 265 270
 Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
 275 280

<210> 97

<211> 831

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (18)..(821)

<400> 97

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                  1                      5                      10

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Ala Phe Ala Gly Lys Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val
                  15                      20                      25

ctt gga agc ggc cgt gtg aca atg agg aag act gtt gcc aag cca aag     146
Leu Gly Ser Gly Arg Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys
                  30                      35                      40

ggc cca tca ggc agc cca tgg tac gga tct gac cgt gtc aag tac ttg     194
Gly Pro Ser Gly Ser Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu
                  45                      50                      55

ggt cca ttc tct ggc gaa tca ccg agc tac ctt acc gga gag ttc ccc     242
Gly Pro Phe Ser Gly Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro
                  60                      65                      70                      75

gga gac tac gga tgg gac acc gcc gga ctt tca gct gac ccc gag aca     290
Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr
                  80                      85                      90

ttc gca agg aac cgt gaa cta gaa gtt atc cac agc agg tgg gct atg     338
Phe Ala Arg Asn Arg Glu Leu Glu Val Ile His Ser Arg Trp Ala Met
                  95                      100                      105

ctc gga gcc cta ggc tgc gtc ttc cct gag ctt ttg gct aga aac gga     386
Leu Gly Ala Leu Gly Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly
                  110                      115                      120

gtc aag ttc gga gag gcg gtt tgg ttc aag gcc ggt tca cag atc ttc     434
Val Lys Phe Gly Glu Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe
                  125                      130                      135

agc gat gga ggg ctc gat tac ttg gga aac cct agc ttg gtt cac gct     482
Ser Asp Gly Gly Leu Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala
                  140                      145                      150                      155

cag agc att ttg gcc att tgg gcc aca caa gtt att ttg atg gga gcc     530
Gln Ser Ile Leu Ala Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala
                  160                      165                      170

gtt gaa ggc tac aga gtc gca gga aat ggg cca ttg gga gag gcc gag     578
Val Glu Gly Tyr Arg Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu
                  175                      180                      185

gac ttg ctt tac ccc ggt ggc agc ttc gac cca ttg ggt ttg gct acc     626
Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr
                  190                      195                      200

gac cca gag gca ttc gct gag ttg aag gtg aag gag ctc aag aac gga     674

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Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly
 205 210 215
 aga ttg gct atg ttc tct atg ttt gga ttc ttc gtt caa gcc atc gtc 722
 Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val
 220 225 230 235
 act ggt aag gga ccg ata gag aac ctt gct gac cat ttg gcc gat cca 770
 Thr Gly Lys Gly Pro Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro
 240 245 250
 gtt aac aac aac gca tgg gcc ttc gcc acc aac ttt gtt ccc gga aag 818
 Val Asn Asn Asn Ala Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys
 255 260 265
 tga gccaaagtttt 831

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<400> 98
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 20 25 30
 Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys Gly Pro Ser Gly Ser
 35 40 45
 Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu Gly Pro Phe Ser Gly
 50 55 60
 Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro Gly Asp Tyr Gly Trp
 65 70 75 80
 Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Arg Asn Arg
 85 90 95
 Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly
 100 105 110
 Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly Val Lys Phe Gly Glu
 115 120 125
 Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Asp Gly Gly Leu
 130 135 140
 Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala Gln Ser Ile Leu Ala
 145 150 155 160
 Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala Val Glu Gly Tyr Arg
 165 170 175

Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu Asp Leu Leu Tyr Pro
 180 185 190

Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr Asp Pro Glu Ala Phe
 195 200 205

Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly Arg Leu Ala Met Phe
 210 215 220

Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val Thr Gly Lys Gly Pro
 225 230 235 240

Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro Val Asn Asn Asn Ala
 245 250 255

Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys
 260 265

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 1 5 10

aca gcc act aga aga gtt ctc atc gct ctt cac gag aag aat gtc gac 98
 Thr Ala Thr Arg Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp
 15 20 25

ttt gaa ttc gtt cat gtc gag ctc aaa gat ggt gaa cac aag aaa gag 146
 Phe Glu Phe Val His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu
 30 35 40

cct ttc atc ctt cgc aac gtgagtacat ataacatctg tcaagccaaa 194
 Pro Phe Ile Leu Arg Asn
 45 50

atattgtatt tcattctagat actgaatctt ggtcttaaca atcttgaata atgtttttgc 254

ag ccc ttt ggt aaa gtt cca gcc ttt gaa gat gga gac ttc aag att 301
 Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys Ile
 55 60 65

ttc g gtaaatacaa atatatatca ttatagtcac gtttacaaat ttttggtttt 355
 Phe G

atgatcattg caataataga aagcagaaac actcaaaaat gttttttttt tgggtgggcag 415

aa tca aga gca att act caa tac ata gct cat gaa ttc tca gac aaa 462
 lu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser Asp Lys
 70 75 80

gga aac aac ctt ctc tca act ggc aag gac atg gcg atc ata gcc atg 510
 Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile Ala Met
 85 90 95

ggc att gaa att gag tcg cat gag ttt gac cca gtt ggt tca aag ctt 558
 Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser Lys Leu
 100 105 110

gtt tgg gag caa gtc tta aag cct ttg tat ggt atg acc aca gac aaa 606
 Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr Asp Lys
 115 120 125

act gtt gtt gaa gaa gaa gag gct aag cta gcc aaa gtc ctc gat gtt 654
 Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu Asp Val
 130 135 140 145

tac gaa cac agg ctt ggt gag tcc aag tat ttg gct tct gac cac ttc 702
 Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp His Phe
 150 155 160

act ttg gtc gat ctt cac act atc cct gtg att caa tac tta ctt gga 750
 Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu Leu Gly
 165 170 175

act cca act aag aaa ctc ttc gac gag cgt cca cat gtg agt gct tgg 798
 Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser Ala Trp
 180 185 190

gtt gct gac atc act tca agg cct tct gct cag aag gtt ctt taa 843
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 195 200 205

gtgaatctca aa 855

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 <213> Arabidopsis thaliana

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 20 25 30
 His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu Pro Phe Ile Leu
 35 40 45
 Arg Asn Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys
 50 55 60
 Ile Phe Glu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser
 65 70 75 80
 Asp Lys Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile
 85 90 95
 Ala Met Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser
 100 105 110
 Lys Leu Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr
 115 120 125
 Asp Lys Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu
 130 135 140
 Asp Val Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp
 145 150 155 160
 His Phe Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu
 165 170 175
 Leu Gly Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser
 180 185 190
 Ala Trp Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu
 195 200 205

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 1 5 10
 acc gct ggc aaa gct ga ggtactactc tttctctctt tgacagaact 97
 Thr Ala Gly Lys Ala Gl
 15
 cttaaactgg aaaaattggt gaagctataa ctctttgaaa acagttgaaa cttgatcatt 157
 actagaaatt tcagttactt gtttaattta gtttgctgta attatgtaat tgatgatttt 217
 atggttacaa tgggtgcat gta g gag aag agc aat gtt ctg ctg gac aag 268
 u Glu Lys Ser Asn Val Leu Leu Asp Lys
 20 25
 gcc aag gat gct gca gct ggt gct gga gct gga gca caa ca ggtaaacaat 319
 Ala Lys Asp Ala Ala Ala Gly Ala Gly Ala Gln Gl
 30 35 40
 ccatacacag acacataaca tataatatgt aacgaaataa acgtctttgt aagcttacat 379
 gtacgcagat ttctgatatg gttatgtata tggtata g gcg gga aag agt gta 432
 n Ala Gly Lys Ser Val
 45
 tcg gat gcg gca gcg gga ggt gtt aac ttc gtg aag gac aag acc ggc 480
 Ser Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly
 50 55 60
 ctg aac aag tag agattcgggt caaatttggg 512
 Leu Asn Lys
 65

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 <211> 66
 <212> PRT
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 35 40 45
 Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly Leu
 50 55 60
 Asn Lys
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<220>
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 <222> (11)..(1123)

<400> 103

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              1              5              10

gaa ggg aag cat tac ttc tca atg tgg caa act ctg ttc gag atc gac      97
Glu Gly Lys His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp
      15              20              25

act aag tac atg cct atc aag cct att ggt cgt gga gct tac ggt gtt      145
Thr Lys Tyr Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val
      30              35              40              45

gtc tgc tcc tct gtt aac agt gac acc aac gag aaa gtt gct atc aag      193
Val Cys Ser Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys
              50              55              60

aag att cac aat gtt tat gag aat agg atc gat gcg ttg agg act ctt      241
Lys Ile His Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu
              65              70              75

cgg gag ctc aag ctt cta cgc cat ctt cga cat gag aat gtc att gct      289
Arg Glu Leu Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala
              80              85              90

ttg aaa gat gtc atg atg cca att cat aag atg agc ttc aag gat gtt      337
Leu Lys Asp Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val
              95              100              105

tat ctt gtt tat gag ctc atg gac act gat ctc cac cag att atc aag      385
Tyr Leu Val Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys
      110              115              120              125

tct tct cag cgt ctt agt aac gat cat tgc caa tac ttc ttg ttc cag      433
Ser Ser Gln Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln
              130              135              140

ttg ctt cga ggg ctc aag tat att cat tca gcc aat atc ctg cac cga      481
Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg
              145              150              155

gat ttg aaa cct ggt aac ctt ctt gtc aac gca aac tgc gat tta aag      529
Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys
              160              165              170

ata tgc gat ttt gga cta gcg cgt gcg agc aac acc aag ggt cag ttc      577
Ile Cys Asp Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe
      175              180              185

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atg act gaa tat gtt gtg act cgt tgg tac cga gcc cca gag ctt ctc 625
 Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
 190 195 200 205

ctc tgt tgt gac aac tat gga aca tcc att gat gtt tgg tct gtt ggt 673
 Leu Cys Cys Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly
 210 215 220

tgc att ttc gcc gag ctt ctt ggt agg aaa ccg ata ttc caa gga acg 721
 Cys Ile Phe Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr
 225 230 235

gaa tgt ctt aac cag ctt aag ctc att gtc aac att atc gga agc caa 769
 Glu Cys Leu Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln
 240 245 250

aga gaa gaa gat ctt gag ttc ata gtt aac ccg aaa gct aaa aga tac 817
 Arg Glu Glu Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr
 255 260 265

att aga tca ctt ccg tac tca cct ggg atg tct tta tcc aga ctt tac 865
 Ile Arg Ser Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr
 270 275 280 285

ccg tgc gct cat gta ttg gcc atc gac ctt ctg cag aaa atg ctt gtt 913
 Pro Cys Ala His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val
 290 295 300

ttt gat ccg tca aag agg att agt gcc tct gaa gca ctc cag cat cca 961
 Phe Asp Pro Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro
 305 310 315

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 Tyr Met Ala Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val
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cct atc gat ctc gat gta gat gag gat ttg aga gag gag atg ata aga 1057
 Pro Ile Asp Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg
 335 340 345

gaa atg ata tgg aat gag atg ctt cac tac cat cca caa gct tca acc 1105
 Glu Met Ile Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr
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<212> PRT

<213> Arabidopsis thaliana

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Met Pro Ile	Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val Val Cys Ser		
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Ser Val Asn	Ser Asp Thr Asn Glu Lys Val Ala Ile Lys Lys Ile His		
	50	55	60
Asn Val Tyr	Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu Arg Glu Leu		
	65	70	75
Lys Leu Leu	Arg His Leu Arg His Glu Asn Val Ile Ala Leu Lys Asp		
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Val Met Met	Pro Ile His Lys Met Ser Phe Lys Asp Val Tyr Leu Val		
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Tyr Glu Leu	Met Asp Thr Asp Leu His Gln Ile Ile Lys Ser Ser Gln		
	115	120	125
Arg Leu Ser	Asn Asp His Cys Gln Tyr Phe Leu Phe Gln Leu Leu Arg		
	130	135	140
Gly Leu Lys	Tyr Ile His Ser Ala Asn Ile Leu His Arg Asp Leu Lys		
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Pro Gly Asn	Leu Leu Val Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp		
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Phe Gly Leu	Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe Met Thr Glu		
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Tyr Val Val	Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys		
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Asp Asn Tyr	Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe		
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Ala Glu Leu	Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr Glu Cys Leu		
	225	230	235
Asn Gln Leu	Lys Leu Ile Val Asn Ile Ile Gly Ser Gln Arg Glu Glu		
	245	250	255
Asp Leu Glu	Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr Ile Arg Ser		
	260	265	270
Leu Pro Tyr	Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr Pro Cys Ala		
	275	280	285
His Val Leu	Ala Ile Asp Leu Leu Gln Lys Met Leu Val Phe Asp Pro		
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Ala	Lys	Thr	Met	Ala	Ala	Asn	Lys	Asp	Lys	Asp	Lys	Asp	Lys	Lys	Lys		
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Pro	Ile	Ser	Arg	Ser	Ala	Arg	Ala	Gly	Ile	Gln	Phe	Pro	Val	Gly	Arg		
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Ala	Thr	Ala	Ala	Val	Tyr	Thr	Ala	Ser	Ile	Leu	Glu	Tyr	Leu	Thr	Ala		
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gag	gtt	ctt	gag	ttg	gct	ggg	aat	gcg	agc	aag	gat	ctc	aaa	gtg	aag		292
Glu	Val	Leu	Glu	Leu	Ala	Gly	Asn	Ala	Ser	Lys	Asp	Leu	Lys	Val	Lys		
				80					85					90			
agg	ata	acg	cca	agg	cat	ctg	cag	ttg	gcg	att	aga	gga	gat	gag	gag		340
Arg	Ile	Thr	Pro	Arg	His	Leu	Gln	Leu	Ala	Ile	Arg	Gly	Asp	Glu	Glu		
			95					100					105				
ctg	gac	aca	ctc	atc	aag	gga	acg	att	gct	gga	ggt	ggt	gtg	atc	cct		388
Leu	Asp	Thr	Leu	Ile	Lys	Gly	Thr	Ile	Ala	Gly	Gly	Gly	Val	Ile	Pro		
		110					115					120					

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 Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu
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 Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg
 85 90 95
 His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile
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Tyr Asp Pro Leu His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu	
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Ala Lys Ser Thr Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg	
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aaa acc att tca aga gaa atg ttc ttc ttc aac ccg ttt act cgt gag	193
Lys Thr Ile Ser Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu	
45 50 55 60	
ctc ata aac gta cca aaa tgt act tta tca tat gat gcg atc gct ttc	241
Leu Ile Asn Val Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe	
65 70 75	
tct tgt gca cct aca tca ggt act tgc gtg ttg cta gca ttt aag cat	289
Ser Cys Ala Pro Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His	
80 85 90	
gtt tgc tat cgt atc acc act acg agc act tgc cat ccc aaa gca acc	337
Val Ser Tyr Arg Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr	
95 100 105	
gag tgg gtt act gag gat cta caa ttc cat cgt cgc ttc cgc agt gaa	385
Glu Trp Val Thr Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu	
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aca ctt aac cac agc aat gtt gtc tat gcc aaa cgt cgc ttc tat tgc	433
Thr Leu Asn His Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys	
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ctt gac ggt caa gga agc tta tat tac ttt gat ccg tct tct cga aga	481
Leu Asp Gly Gln Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg	
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Trp Asp Phe Ser Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp	
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Arg Phe Ser Tyr Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala	
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Val Arg Lys Gly Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys	
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ccg ata gtg cat aag tta gaa gat atc aat tgg gag gag atc aat agt	673
Pro Ile Val His Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser	
205 210 215 220	
act acg att gat gga ttg aca atc ttt acg ggt ctt tat tcc tct gag	721
Thr Thr Ile Asp Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu	
225 230 235	
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 Leu Arg Phe Asn Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu
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 Arg Tyr Tyr Pro Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro
 270 275 280
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 Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe Ser Cys Ala Pro
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 Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His Val Ser Tyr Arg
 85 90 95
 Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr Glu Trp Val Thr
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 Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg Trp Asp Phe Ser
 145 150 155 160
 Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp Arg Phe Ser Tyr
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Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala Val Arg Lys Gly
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 210 215 220
 Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu Val Arg Leu Asn
 225 230 235 240
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 245 250 255
 Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu Arg Tyr Tyr Pro
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gatacctaaa ccaaataccaa ttca atg gcg gaa gaa gca aaa tcc aaa gga	171
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Asn Ala Ala Phe Ser Ser Gly Asp Tyr Ala Thr Ala Ile Thr His Phe	
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aca gaa gca atc aac ctt tca cca acc aat cac atc ctc tac tca aac	267
Thr Glu Ala Ile Asn Leu Ser Pro Thr Asn His Ile Leu Tyr Ser Asn	
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aga tcc gct tct tac gct tct ctc cac cgt tac gaa gaa gct tta tca	315
Arg Ser Ala Ser Tyr Ala Ser Leu His Arg Tyr Glu Glu Ala Leu Ser	
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gac gcg aag aag act ata gag ctt aaa cct gat tgg tct aaa gga tat	363
Asp Ala Lys Lys Thr Ile Glu Leu Lys Pro Asp Trp Ser Lys Gly Tyr	
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Ser Arg Leu Gly Ala Ala Phe Ile Gly Leu Ser Lys Phe Asp Glu Ala	
75 80 85	
gtt gat tcg tat aag aaa gga tta gag att gat ccg agt aat gag atg	459
Val Asp Ser Tyr Lys Lys Gly Leu Glu Ile Asp Pro Ser Asn Glu Met	
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Leu Lys Ser Gly Leu Ala Asp Ala Ser Arg Ser Arg Val Ser Ser Lys	
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Ser Asn Pro Phe Val Asp Ala Phe Gln Gly Lys Glu Met Trp Glu Lys	
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Leu Thr Ala Asp Pro Gly Thr Arg Val Tyr Leu Glu Gln Asp Asp Phe	
140 145 150	
gtt aag acg atg aag gag att cag agg aac cct aat aat ctt aat ttg	651
Val Lys Thr Met Lys Glu Ile Gln Arg Asn Pro Asn Asn Leu Asn Leu	
155 160 165	
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Tyr Met Lys Asp Lys Arg Val Met Lys Ala Leu Gly Val Leu Leu Asn	
170 175 180 185	
gtg aag ttt ggt gga tct agt ggt gaa gat act gag atg aag gag gct	747
Val Lys Phe Gly Gly Ser Ser Gly Glu Asp Thr Glu Met Lys Glu Ala	
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Asp Glu Arg Lys Glu Pro Glu Pro Glu Met Glu Pro Met Glu Leu Thr	
205 210 215	
gag gag gag agg cag aag aag gag aga aag gag aag gct ttg aag gag	843

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202

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 Tyr Ser Asn Arg Ala Ala Cys Tyr Thr Lys Leu Gly Ala Leu Pro Glu
 410 415 420
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 Gly Leu Lys Asp Ala Glu Lys Cys Ile Glu Leu Asp Pro Ser Phe Thr
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Val Gln Val Arg
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65 70 75 80
Ile Gly Leu Ser Lys Phe Asp Glu Ala Val Asp Ser Tyr Lys Lys Gly
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Leu Glu Ile Asp Pro Ser Asn Glu Met Leu Lys Ser Gly Leu Ala Asp
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Phe Gln Gly Lys Glu Met Trp Glu Lys Leu Thr Ala Asp Pro Gly Thr
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Arg Val Tyr Leu Glu Gln Asp Asp Phe Val Lys Thr Met Lys Glu Ile
145 150 155 160
Gln Arg Asn Pro Asn Asn Leu Asn Leu Tyr Met Lys Asp Lys Arg Val
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Met Lys Ala Leu Gly Val Leu Leu Asn Val Lys Phe Gly Gly Ser Ser
180 185 190
Gly Glu Asp Thr Glu Met Lys Glu Ala Asp Glu Arg Lys Glu Pro Glu
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Pro Glu Met Glu Pro Met Glu Leu Thr Glu Glu Glu Arg Gln Lys Lys
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Glu Arg Lys Glu Lys Ala Leu Lys Glu Lys Gly Glu Gly Asn Val Ala

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Val Tyr Leu Glu Met Gly Lys Tyr Glu Glu Cys Ile Glu Asp Cys Asp	275		280		285	
Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe Lys Met Ile	290		295		300	
Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys Met Ala Arg	305		310		315	320
Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln Lys Ala Leu	325		330		335	
Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn Asp Ala Glu	340		345		350	
Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp Pro Thr Ile	355		360		365	
Ala Glu Glu Glu Arg Glu Lys Gly Asn Gly Phe Phe Lys Glu Gln Lys	370		375		380	
Tyr Pro Glu Ala Val Lys His Tyr Ser Glu Ala Ile Lys Arg Asn Pro	385		390		395	400
Asn Asp Val Arg Ala Tyr Ser Asn Arg Ala Ala Cys Tyr Thr Lys Leu	405		410		415	
Gly Ala Leu Pro Glu Gly Leu Lys Asp Ala Glu Lys Cys Ile Glu Leu	420		425		430	
Asp Pro Ser Phe Thr Lys Gly Tyr Ser Arg Lys Gly Ala Ile Gln Phe	435		440		445	
Phe Met Lys Glu Tyr Asp Lys Ala Met Glu Thr Tyr Gln Glu Gly Leu	450		455		460	
Lys His Asp Pro Lys Asn Gln Glu Phe Leu Asp Gly Val Arg Arg Cys	465		470		475	480
Val Glu Gln Ile Asn Lys Ala Ser Arg Gly Asp Leu Thr Pro Glu Glu	485		490		495	
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Ile Leu Ser Asp Pro Val Met Arg Gln Val Leu Val Asp Phe Gln Glu	515		520		525	
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530

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540

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 Met Gly Arg Ala Pro Cys Cys Asp Lys Ala Asn Val Lys Lys
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27

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gttactcagt ttt tac gta gac gat gtg cca ata aga gaa tac aaa aac 821
Phe Tyr Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn
145 150 155

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Asn Glu Ala Lys Asn Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val
160 165 170

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Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu
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gag aaa att gat tgg agc aaa gct cca ttt tat gct tat tac aaa gat 965
Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp
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Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser
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Asn Pro His Asn Trp Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala
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Val Glu Ala Arg Arg Tyr Arg Trp Val Arg Val Asn His Met Val Tyr
240 245 250

gat tat tgt act gac cgg tct agg ttt cct gtc cca cca ccc gag tgt 1157
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 Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe Tyr Met Asn Ser Asp
 65 70 75 80
 Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Arg
 85 90 95
 Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe Ala His Gly Lys
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 Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp Pro Ser Met Asp
 115 120 125
 Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His Ile Val Phe Tyr
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 Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn Asn Glu Ala Lys Asn
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 Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val Tyr Ser Thr Leu Trp
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 Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu Glu Lys Ile Asp Trp
 180 185 190
 Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp Phe Asp Ile Glu Gly
 195 200 205
 Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser Asn Pro His Asn Trp
 210 215 220
 Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala Val Glu Ala Arg Arg
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Ile Arg Arg Thr Leu Thr Lys Pro His Gly Thr Phe Ser Arg Cys Arg
10 15 20 25

tac tta tca acc gcc gct gct gcg acg gag gtg aat tac gag gat gaa 147
Tyr Leu Ser Thr Ala Ala Ala Ala Thr Glu Val Asn Tyr Glu Asp Glu
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tcg att atg atg aaa gga gtt cga att tca ggt aga cct ctt tac tta 195
Ser Ile Met Met Lys Gly Val Arg Ile Ser Gly Arg Pro Leu Tyr Leu
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Asp Met Gln Ala Thr Thr Pro Ile Asp Pro Arg Val Phe Asp Ala Met
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Asn Ala Ser Gln Ile His Glu Tyr Gly Asn Pro His Ser Arg Thr His
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ctc tac ggc tgg gaa gct gag aac gcc gtc gag aac gca cga aac cag 339
Leu Tyr Gly Trp Glu Ala Glu Asn Ala Val Glu Asn Ala Arg Asn Gln
90 95 100 105

gtc gcg aaa ctg atc gaa gct tca ccg aag gag atc gta ttc gtg tcc 387
Val Ala Lys Leu Ile Glu Ala Ser Pro Lys Glu Ile Val Phe Val Ser
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Gly Ala Thr Glu Ala Asn Asn Met Ala Val Lys Gly Val Met His Phe
125 130 135

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Tyr Lys Asp Thr Lys Lys His Val Ile Thr Thr Gln Thr Glu His Lys
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Cys Val Leu Asp Ser Cys Arg His Leu Gln Gln Glu Gly Phe Glu Val
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Thr Tyr Leu Pro Val Lys Thr Asp Gly Leu Val Asp Leu Glu Met Leu
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Arg Glu Ala Ile Arg Pro Asp Thr Gly Leu Val Ser Ile Met Ala Val
190 195 200

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Asn Asn Glu Ile Gly Val Val Gln Pro Met Glu Glu Ile Gly Met Ile
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Gly	Lys	Ile	Pro	Val	Asp	Val	Lys	Lys	Trp	Asn	Val	Ala	Leu	Met	Ser	
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Arg	Glu	Lys	Leu	Asp	Gly	Val	Val	Val	Asn	Gly	Ser	Met	Asp	Ser	Arg	
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Tyr	Val	Gly	Asn	Leu	Asn	Leu	Ser	Phe	Ala	Tyr	Val	Glu	Gly	Glu	Ser	
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Leu	Leu	Met	Gly	Leu	Lys	Glu	Val	Ala	Val	Ser	Ser	Gly	Ser	Ala	Cys	
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Thr	Ser	Ala	Ser	Leu	Glu	Pro	Ser	Tyr	Val	Leu	Arg	Ala	Leu	Gly	Val	
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Asp	Glu	Asp	Met	Ala	His	Thr	Ser	Ile	Arg	Phe	Gly	Ile	Gly	Arg	Phe	
	395					400					405					
acc	acg	aag	gaa	gag	att	gat	aaa	gcg	gtc	gag	ctt	acg	gtt	aaa	caa	1299
Thr	Thr	Lys	Glu	Glu	Ile	Asp	Lys	Ala	Val	Glu	Leu	Thr	Val	Lys	Gln	
410					415					420					425	
gtt	gag	aag	ttg	agg	gaa	atg	agc	ccg	ctt	tat	gaa	atg	gtt	aaa	gaa	1347
Val	Glu	Lys	Leu	Arg	Glu	Met	Ser	Pro	Leu	Tyr	Glu	Met	Val	Lys	Glu	
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1399

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Arg Ile Ser Gly Arg Pro Leu Tyr Leu Asp Met Gln Ala Thr Thr Pro
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Ile Asp Pro Arg Val Phe Asp Ala Met Asn Ala Ser Gln Ile His Glu
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Tyr Gly Asn Pro His Ser Arg Thr His Leu Tyr Gly Trp Glu Ala Glu
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Ser Pro Lys Glu Ile Val Phe Val Ser Gly Ala Thr Glu Ala Asn Asn
 115 120 125

Met Ala Val Lys Gly Val Met His Phe Tyr Lys Asp Thr Lys Lys His
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Val Ile Thr Thr Gln Thr Glu His Lys Cys Val Leu Asp Ser Cys Arg
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His Leu Gln Gln Glu Gly Phe Glu Val Thr Tyr Leu Pro Val Lys Thr
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Asp Gly Leu Val Asp Leu Glu Met Leu Arg Glu Ala Ile Arg Pro Asp
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Thr Gly Leu Val Ser Ile Met Ala Val Asn Asn Glu Ile Gly Val Val
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Gln Pro Met Glu Glu Ile Gly Met Ile Cys Lys Glu His Asn Val Pro
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att	gat	ctc	tcc	ggc	tat	aat	atc	tcc	ggg	ggc	ttt	ccc	tac	gga	ttc	289
Ile	Asp	Leu	Ser	Gly	Tyr	Asn	Ile	Ser	Gly	Gly	Phe	Pro	Tyr	Gly	Phe	
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Cys	Arg	Ile	Arg	Thr	Leu	Ile	Asn	Ile	Thr	Leu	Ser	Gln	Asn	Asn	Leu	
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Asn	Leu	Ile	Leu	Asn	Gln	Asn	Asn	Phe	Ser	Gly	Lys	Leu	Pro	Glu	Phe	
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Ser	Pro	Glu	Phe	Arg	Lys	Leu	Arg	Val	Leu	Glu	Leu	Glu	Ser	Asn	Leu	
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Ser Ile Met Asn Leu Val Leu Leu Glu Asn Leu Asp Leu Ala Met Asn	
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Ser Leu Thr Gly Glu Ile Pro Glu Ser Ile Gly Arg Leu Glu Ser Val	
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Leu Cys Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln	
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Gln Leu Glu Ile Ser Ala Asn Asn Phe Ser Gly Val Ile Pro Val Lys	
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Asn Pro Asn Leu Cys Ala Pro Asn Leu Asp Pro Ile Arg Pro Cys Arg	
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Ser Lys Arg Glu Thr Arg Tyr Ile Leu Pro Ile Ser Ile Leu Cys Ile	
610 615 620	
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Val Ala Leu Thr Gly Ala Leu Val Trp Leu Phe Ile Lys Thr Lys Pro	
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Lys Ser Gly Gln Thr Leu Ala Val Lys Lys Leu Trp Gly Glu Thr Gly	
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Val Lys Ser Asn Asn Ile Leu Leu Asp His Glu Met Lys Pro Arg Val	
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Ala Pro G	
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 930 935 940
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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 15/82, 15/10, 9/12, 5/10, C12Q 1/68, A01H 5/00	A3	(11) International Publication Number: WO 00/08187 (43) International Publication Date: 17 February 2000 (17.02.00)
(21) International Application Number: PCT/EP99/05652 (22) International Filing Date: 4 August 1999 (04.08.99) (30) Priority Data: 98202634.6 4 August 1998 (04.08.98) EP (71) Applicant (for all designated States except US): VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECH- NOLOGIE [BE/BE]; Rijvisschestraat 120, B-9052 Zwij- naarde (BE). (72) Inventors; and (75) Inventors/Applicants (for US only): LEE, Jeong, Hee [KR/BE]; Spinnmolenplein 274 (22K), B-9000 Gent (BE). VERBRUGGEN, Nathalie [BE/BE]; Avenue des Saisons, 53, B-1050 Ixelles (BE). (74) Agent: DE CLERCQ, Ann; Ann De Clercq & Co. B.V.B.A., Brandstraat 100, B-9830 Sint-Martens-Latem (BE).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> (88) Date of publication of the international search report: 29 June 2000 (29.06.00)
(54) Title: GENES INVOLVED IN TOLERANCE TO ENVIRONMENTAL STRESS (57) Abstract <p>The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table I as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.</p>		

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DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 99/05652

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/82 C12N15/10 C12N9/12 C12N5/10 C12Q1/68
A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	PRÄNDL, R., ET AL. : "HSF3, a new heat shock factor from Arabidopsis thaliana, derepresses the heat shock response and confers thermotolerance when overexpressed in transgenic plants" MOLECULAR AND GENERAL GENETICS, vol. 258, May 1998 (1998-05), pages 269-278, XP002135096 the whole document --- -/--	2,3,7,8, 11-14, 16,18, 21, 24-26, 28-37



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents :

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- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

10 April 2000

Date of mailing of the International search report

27.04.00

Name and mailing address of the ISA

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Fax: (+31-70) 340-3016

Authorized officer

Holtorf, S

INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 99/05652

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KUSHNIR, S., ET AL.: "characterization of Arabidopsis thaliana cDNAs that render yeasts tolerant toward the thiol-oxidizing drug diamide" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE USA, vol. 92, November 1995 (1995-11), pages 10580-10584, XP002127804 see also last paragraph the whole document ---	1,2
Y	WO 96 39020 A (UNIV CALIFORNIA) 12 December 1996 (1996-12-12) the whole document ---	1,2
Y	QUINTERO, F.J., ET AL.: "the SAL1 gene of Arabidopsis, encoding an enzyme with 3' (2'),5'-bisphosphate nucleotidase and inositol polyphosphate 1-phosphatase activities, Increases salt tolerance in yeast" THE PLANT CELL, vol. 8, March 1996 (1996-03), pages 529-537, XP002092755 see last paragraph the whole document ---	1,2
Y	BABIYCHUK, E., ET AL.: "Arabidopsis thaliana NADPH oxidoreductase homologs confer tolerance of yeasts towards the thiol-oxidizing drug Diamide" THE JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 270, no. 44, 1995, pages 26224-26231, XP002127805 see last paragraph the whole document ---	1,2
Y	GIRAUDAT J ET AL: "ISOLATION OF THE ARABIDOPSIS AB13 GENE BY POSITIONAL CLONING" PLANT CELL, US, AMERICAN SOCIETY OF PLANT PHYSIOLOGISTS, ROCKVILLE, MD, vol. 4, 1 October 1992 (1992-10-01), pages 1251-1261, XP002063682 ISSN: 1040-4651 the whole document ---	1,2
Y	WO 97 41152 A (UNIV NEW YORK) 6 November 1997 (1997-11-06) page 59, line 1 - line 5 ---	1,2

-/--

INTERNATIONAL SEARCH REPORT

Int. Patent Application No.
PCT/EP 99/05652

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	NAMBARA, E., ET AL.: "a mutant of Arabidopsis which is defective in seed development and storage protein accumulation is a new abi3 allele" THE PLANT JOURNAL, vol. 2, no. 4, 1992, pages 435-441, XP002129247 the whole document ----	1,2
A	HELM, K.W. AND VIERLING, E.: "an Arabidopsis thaliana cDNA clone encoding a low molecular weight heat shock protein" NUCLEIC ACID RESEARCH, vol. 17, no. 19, 1989, page 7995 XP002129295 the whole document ----	1,2
A	YANG H ET AL: "Arabidopsis thaliana ECP63 encoding a LEA protein is located in chromosome 4" GENE: AN INTERNATIONAL JOURNAL ON GENES AND GENOMES, GB, ELSEVIER SCIENCE PUBLISHERS, BARKING, vol. 184, no. 1, 3 January 1997 (1997-01-03), pages 83-88, XP004093225 ISSN: 0378-1119 the whole document ----	1,2
A	MIZOGUSHI, T., ET AL.: "characterization of two cDNAs that encode MAP kinase homologues in Arabidopsis thaliana and analysis of the possible role of auxin in activating such kinase activities in cultured cells" THE PLANT JOURNAL, vol. 5, no. 1, 1994, pages 111-122, XP002129296 the whole document ----	1,2
P, X	LEE, J.H., ET AL.: "a highly conserved kinase is an essential component for stress tolerance in yeast and plant cells" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE USA, vol. 96, May 1999 (1999-05), pages 5873-5877, XP002127807 the whole document -----	1,2

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP 99/05652

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

1,2-4,7,8,10-14,16-37 (inventions 1,3,37)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claim : 1 completely ; 2 partially

A method to identify cDNAs involved in environmental stress tolerance in plants by expressing a silique-specific cDNA library obtained from said plant in yeast cells and screening the yeast cells for enhanced environmental stress tolerance or resistance.

2. Claims: 5,6,15 completely , 2,3,4,11,12,13,14,
18-37 partially

An isolated cDNA as identified by SEQID 1 coding for a DBF2-related peptide characterized by SEQID 2; furthermore the use of the cDNA in methods to produce transgenic plants with enhanced environmental stress tolerance or resistance.

3. Claims: 10,17 completely , 2,3,4,11,12,13,14,
18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 5 coding for a c74-related peptide characterized by SEQID 6.

4. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 7 coding for a ADH2-related peptide characterized by SEQID 8.

5. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 9 coding for a catalase /catalase3-related peptide characterized by SEQID 10.

6. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 11 coding for a HSP90-related peptide characterized by SEQID 12.

7. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

by SEQID 13 coding for a peptide similar to a phosphoenolpyruvate carboxylase characterized by SEQID 14.

8. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 15 coding for a PR-protein characterized by SEQID 16.

9. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 17 coding for a protein similar to an ascorbate peroxidase characterized by SEQID 18.

10. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 19,21 coding for a protein similar to a phosphatase binding protein characterized by SEQID 20,22.

11. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 23,25 coding for a protein similar to a retinol dehydrogenase characterized by SEQID 24,26.

12. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 27,29 coding for a protein similar to a ribosomal protein characterized by SEQID 28,30.

13. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 31 coding for a protein similar to a protein transporter characterized by SEQID 32.

14. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 33 coding for a protein similar to a peptide transporter characterized by SEQID 34.

15. Claims: 2,3,4,11,12,13,14,18-37 partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as invention 2; but limited to the cDNA as identified by SEQID 35 coding for an LCT1-related protein characterized by SEQID 36.

16. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 37 coding for an CYC1-related protein characterized by SEQID 38.

17. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 39 coding for an OSM1-related protein characterized by SEQID 40.

18. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 41 coding for an CUP1-related protein characterized by SEQID 42.

19. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 43 coding for an RAD7-related protein characterized by SEQID 44.

20. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 45 coding for an apocytochrome b-related protein characterized by SEQID 46.

21. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 47 coding for an LPPL1-related protein characterized by SEQID 48.

22. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 49 coding for a protein similar to an auxin binding protein characterized by SEQID 50.

23. Claims: 2,3,4,11,12,13,14,18-37 partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as invention 2; but limited to the cDNA as identified by SEQID 51 coding for an CBP57-related protein characterized by SEQID 52.

24. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 53 coding for a calcineurin B-related protein characterized by SEQID 54.

25. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 55 coding for a calnexin-related protein characterized by SEQID 56.

26. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 57 coding for a calreticulin-related protein characterized by SEQID 58.

27. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 59,61 coding for a calmodulin-related protein characterized by SEQID 60,62.

28. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 63 coding for a DdMek1-related protein characterized by SEQID 64.

29. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 65 coding for an adenosine kinase-related protein characterized by SEQID 66.

30. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 67 coding for a human tyrosine kinase-related protein characterized by SEQID 68.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

31. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 69 coding for an ice-plant tyrosine kinase-related protein characterized by SEQID 70.

32. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 71 coding for a kinase C receptor-related protein characterized by SEQID 72.

33. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 73 coding for a HAT7-related protein characterized by SEQID 74.

34. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 75 coding for a RSEB-related protein characterized by SEQID 76.

35. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 77 coding for a phosphatase 2C-related protein characterized by SEQID 78.

36. Claims: 2,3,4,11,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 121 potentially coding for a caltractin-related protein.

37. Claims: 7,8,16 completely; 2,3,11,13,14,18-37 partially

Idem as invention 1; but limited to the cDNA as identified by SEQID 3 coding for a HSP17.6-related protein characterized by SEQID 4.

38. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 79,81 coding for a LEA-related protein characterized by SEQID 80,82.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

39. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 83 coding for a protein similar to a PR-protein characterized by SEQID 84.

40. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 85 coding for a peroxidase-related protein characterized by SEQID 86.

41. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 87 coding for a ribosomal protein characterized by SEQID 88.

42. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 89 coding for a SAS1-related protein characterized by SEQID 90.

43. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 91 coding for a AIG2-related protein characterized by SEQID 92.

44. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 93 coding for a MTlc-related protein characterized by SEQID 94.

45. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 95 coding for a IPP2-related protein characterized by SEQID 96.

46. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 97 coding for a chlorophyll a/b binding protein protein characterized by SEQID 98.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

47. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention ; but limited to the cDNA as identified by SEQID 99 coding for glutathione transferase characterized by SEQID 100.

48. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 101 coding for kin1-related protein characterized by SEQID 102.

49. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 103 coding for Atmpk1-related protein characterized by SEQID 104.

50. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 105 coding for H2A-related protein characterized by SEQID 106.

51. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 107 coding for a protein with unknown function as characterized by SEQID 108.

52. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 109 coding for a protein with unknown function as characterized by SEQID 110.

53. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 111 coding for a protein with unknown function as characterized by SEQID 112.

54. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 113 coding for a protein with unknown function as

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

characterized by SEQID 114.

55. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 115 coding for a protein with unknown function as characterized by SEQID 116.

56. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 117 coding for a protein with unknown function as characterized by SEQID 118.

57. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 119 coding for a protein with unknown function as characterized by SEQID 120.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 99/05652

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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		EP 0907660 A	14-04-1999

A tormentor in the quest for plant p53-like proteins

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Abstract Over the past few years the presence of p53-like proteins in plants was frequently reported, by using the monoclonal antibody Pab240. By means of protein purification and screening a cDNA library, a Pab240 cross-reacting protein and a cDNA clone were isolated from barley. Peptide- and DNA-sequence analysis identified one and the same protein: 2-oxoglutarate dehydrogenase. Sequence analysis of 2-oxoglutarate dehydrogenase revealed that the protein contains a perfect Pab240 epitope. In barley, the 110 kDa oxoglutarate dehydrogenase was degraded during isolation to a 53 kDa Pab240 cross-reacting polypeptide, thereby mimicking curiously p53-like properties. © 2002 Federation of European Biochemical Societies. Published by Elsevier Science B.V. All rights reserved.

Key words: 2-Oxoglutarate dehydrogenase; p53; Pab240; Immuno recognition; Barley

1. Introduction

Since the first reports that a mechanism of programmed cell death (PCD) occurs in animal as well as in plant cells, research has been focussed on whether typical pathways leading to PCD are conserved among these two kingdoms. Although the majority of the key proteins involved in PCD pathways are highly conserved in animal cells, only a very limited number of counterparts were identified in plants thus far, based on sequence homology. One of the key regulatory proteins of the mammalian apoptotic machinery is tumour suppressor p53. In mammals it is known that p53 mediates G1 arrest following DNA damage in order to allow DNA repair or, in case of severe DNA damage, to induce apoptosis (recently reviewed by Bargonetti and Manfredi [1]). This dual role makes p53 the guardian of the genome integrity. In spite of the fact that several homologues of animal proto-oncogene and tumour suppressor gene-related proteins, like *c-myc*, *c-fos* and *c-jun*, as well as cell cycle regulatory proteins, like retinoblastoma, were identified in plants [2], a putative plant p53 is still not identified. However, several reports appeared in the past ten years speculating on the presence of a putative p53 in plant cells. By using the monoclonal antibody Pab240, recognising a

five amino acid stretch in the central core of the murine p53, cross-reactivity with polypeptides in the range of 53–100 kDa has been found in *Zea mays* [3,4] and *Pisum sativum* [5,6]. The presence and intensity of these cross-reactive bands were often correlated with DNA repair, especially during seed germination [3–7]. Such a correlation is quite conceivable since it has been established that aged seeds contain high levels of DNA damage, occurring during storage of seeds [8] and aged seeds do have an increased mean germination time relative to their unaged counterparts, probably due to an extension of the G1 phase to allow DNA repair [7]. So if it is a question of the presence of a plant p53 homologue, indeed one expects to find it in this stage of plant development.

In our previous experiments, cross-reactivity with 53, 73 and 110 kDa polypeptides with the Pab240 antibody were found in barley suspension cells as well as in germinating barley seeds (unpublished data). In concert with the results reported from pea and maize [3–6] the intensity of the immunostained bands was increased dramatically during the early stage of germination but also after exposure of the suspension cells to UV-B radiation. In this study these cross-reactive polypeptides were identified from protein purification as well as from isolation of cross-reacting clones from a barley cDNA expression library. Both approaches reveal that the cross-reacting polypeptides are *not* putative plant p53 homologues but 2-oxoglutarate dehydrogenase, a complex-forming enzyme involved in the Krebs cycle but containing an ideal epitope to be recognised by the Pab240 antibody.

2. Materials and methods

2.1. Plant material

Embryonic cell suspensions were from barley (*Hordeum vulgare* L. cv. Igri) immature in vivo embryo-derived callus (12 days after flowering) as described by Korthout et al. [9].

2.2. Protein purification

About 900 g fresh-weight embryonic suspension cells were harvested by filtration over one layer Whatman paper no. 1. The cells were homogenised in a buffer (100 ml for each 100 g cells) containing 25 mM Tris-Cl pH 7.5, 0.44 M sucrose, 10 mM MgCl₂, 1 mM dithiothreitol (DTT), 0.1% (w/v) Triton X-100 and 0.1 mM phenylmethylsulfonyl fluoride (PMSF) using an Ultraturrax (Janke and Kunkel, Staufen, Germany; three pulses at 24000 rpm of 30 s intervals). The homogenate was filtrated over two layers of cheesecloth and subsequently centrifuged for 5 min at 600×g to obtain the cellular debris and 20 min at 50000×g to obtain the cytosolic extract. Hence, Pab240 reactive protein(s) were isolated from the cytosolic extract by a three-step purification protocol. The first step consists of ammonium sulphate precipitation. All Pab240 reactive proteins precipitate 55–65% of saturated ammonium sulphate. After dialysis (o/n at 4°C against a buffer containing 25 mM Tris-Cl pH 7.5, 1 mM DTT and 0.1 mM PMSF, using Spectra/por 25 mm cellulose dialyse tubing;

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m.w. cut-off 12 000-14 000; Spectrum Medical Industries, Los Angeles, CA, USA) the dialysate was loaded on a 6 ml Resource-Q column connected to a FPLC-system (Amersham Biosciences, Uppsala, Sweden). Pab240 reactive proteins were eluted between 0.40 and 0.45 M NaCl in dialyse buffer. The Pab240 reactive proteins were further purified by means of preparative SDS-PAGE and fractions containing proteins with molecular masses ranging between 105 and 125 kDa were collected. These fractions were pooled, concentrated by means of ultra-filtration (Diaflow 10YM30 ultra-filtration membranes, Amicon Corporation, Beverly, MA, USA) and dialysed against a buffer containing 25 mM Tris-Cl pH 7.5 and 5 mM EDTA (o/n 4°C). Thereafter ATP was added to a final concentration of 6 mM and the proteins were digested with trypsin (20 µg/ml, 50 min, 23°C). The digest was subjected to SDS-PAGE and the 73 and 53 kDa polypeptide Pab240 cross-reacting bands excised from gel and used for sequence analysis.

2.3. Screening of barley expression library with Pab240

An expression cDNA library was constructed by using λZAP Express[®] vectors according to the manufacturer's instructions (Stratagene, La Jolla, CA, USA). Total mRNA was isolated from a mixture of heat-shocked (30 min, 42°C, 24 h recovery) and control barley embryonic suspension cells. The mRNA was converted to cDNA and packed into λZAP Express[®] vectors. The vectors were tested on the presence of multiple-sized inserts. The average size was about 0.5-2 kbp.

Immunological screening of the expression library with Pab240 was performed as described by Sambrook et al. [10], starting with twelve 150 mm plates containing approximately 50 000 plaque forming units each. About 50-100 positive clones per plate were obtained after the first screen. After purification and isolation of Pab240 immuno-reactive λ-clones, the pBCKMV vectors containing the inserts were excised from the λ-clones according to the manufacturer's instructions and subjected to sequence analysis.

2.4. Electrophoretic separation and Western blot analysis

Samples for protein analysis were separated on a 10% SDS-PAGE gel according to Laemmli [11]. The proteins were electro-transferred to a nitrocellulose membrane (Schleicher and Schuell). For Western analysis the monoclonal antibody Pab240 (sc-99, Santa Cruz Biotechnology, Santa Cruz, CA, USA) was used. Visualisation was performed with goat-anti-mouse horseradish peroxidase (HRP) conjugate (Promega, Madison, WI, USA) followed by chemoluminescent detection.

Preparative electrophoresis was performed by using a Prep-Cell (model 491, Bio-Rad Laboratories, Hercules, CA, USA) on a 75 ml 6% polyacrylamide gel. During the run (at 40 mA/h) fractions of 9 ml were collected and analysed on SDS-PAGE and Western blotting.

2.5. Protein sequence analysis

Polypeptides excised from gel were digested in gel with trypsin extracted from gel and separated by means of preparative high-performance liquid chromatography (HPLC). The amino acid sequence analysis of the peptides was performed by means of N-terminal protein sequence analysis by using an Applied Biosystems Model 494 Procise Protein Sequencing System, on-line connected to an RP-HPLC unit for identification of the step-wise released PTH amino acids.

Sequence analysis was performed by Eurosequence (Groningen, The Netherlands).

3. Results

For studying the presence of p53-like proteins in plant cells, several antibodies were used. Among them the monoclonal Pab240, an antibody originally generated in monoclonal hybridomas from a mouse immunised with a β-galactosidase/murine-p53 fusion protein [12]. By epitope mapping it was

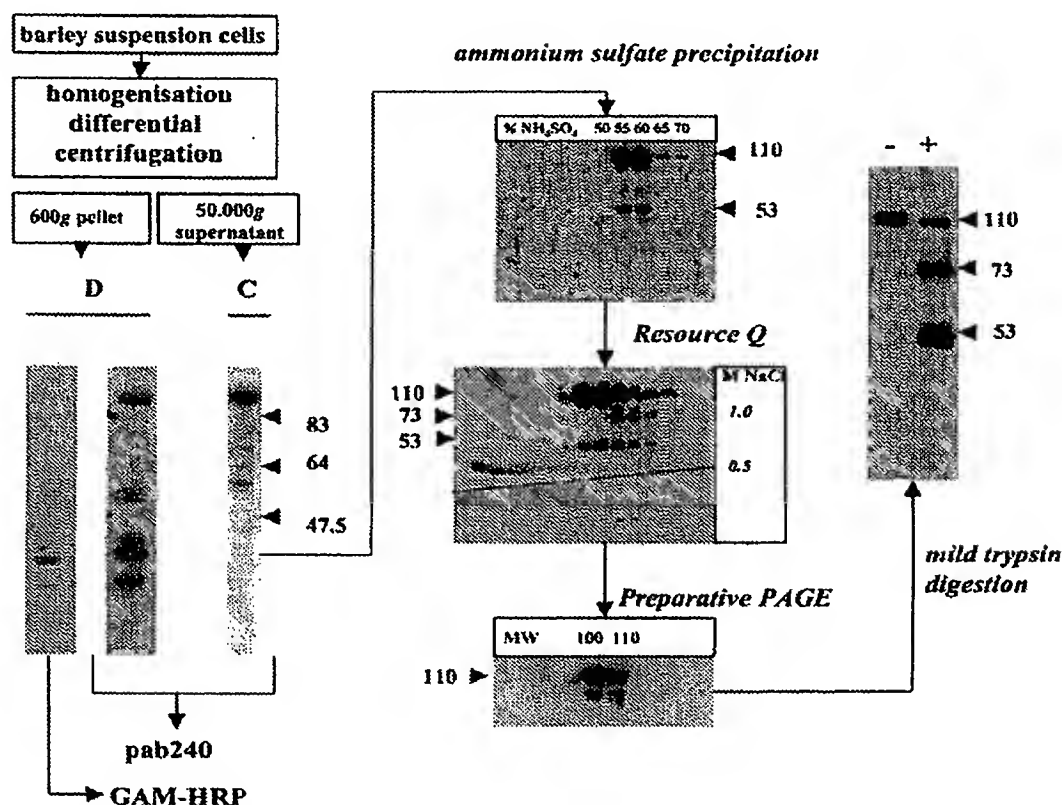


Fig. 1. Purification protocol for the isolation of the 110 kDa Pab240 cross-reactive polypeptide from barley embryonic suspension cells. After differential centrifugation, a 600×g pellet was obtained consisting of cellular debris (D; organelles and nuclei) and a 50 000×g supernatant containing the cytosolic fraction (C). The cytosolic fraction was subjected to a purification protocol comprising ammonium sulphate precipitation, anion exchange (Resource Q) and Preparative PAGE as described in Section 2. Fractions were collected and analysed on Western blots. The 110 kDa polypeptide (–) was subjected to mild trypsin digestion (+) and the 73 and 53 kDa bands were excised from gel and used for sequence analysis. The antibody utilised in all blots was Pab240. Non-specific cross-reaction caused by the secondary antibody (GAM-HRP) was found mainly to be present in the cellular debris.

At-ox:	1	MVWFRIGSSVAKLAIPRTLSQSRCSYATRTRVLPCQTRCFIISTILKSKAESAAPVPRPV	60
At-ox:	61	PLSKLTDSFLDGTSSVYLEELQRAWEADPNVDESNDNFRNFVQGASTSPGISGQTIE	120
At-ox:	121	SMRLLLLVRAYQVNGHMKAKLDPLGLEKREIPEDLTPGLYGFTADLDREFFLGVMRMSG	180
B-p-ox:		M+G MAG	3
At-ox:	181	FLSENRPVQTLRSILSRLEQAYCGTIGYEYMHADRDKNWLRDKIETPTPROYNSERRM	240
B-p-ox:	4	FLSENRPVQTLRSILSRLEQAYCGTIGYEYMHADRDKNWLRDKIETPTPROYNSERRM	63
At-ox:	241	VIYDRLTWSTQFENFLATKWTAKRPGLEGAESLIPGMKEMFDRSADLGVENIVIGMPHR	300
B-p-ox:	64	VMLDRIIWTQFENFLAQKWTAKRPGLEGAETLIPGMKEMFDRSADLGVENIVIGMPHR	123
At-ox:	301	GRNLVGNVVRKPLRQIFSEFSGGT·PV·E GLYTGTDVVKYHLGTSYDRPTRGGKHLH	360
B-p-ox:	124	GRNLVGNVVRKPLRQIFSEFSGGT·PV·E GLYTGTDVVKYHLGTSYDRPTRGGKHLH	183
At-ox:	361	LSLVANPSHLEAVDPVVGKTRAKQYTTDENRTKNMGILIHGDGSFAGQGVVYETLHLS	420
B-p-ox:	184	LSLVANPSHLEAVDPVVGKTRAKQYTTDENRTKNMGILIHGDGSFAGQGVVYETLHLS	243
At-ox:	421	ALPNYCTGCTVHIVVNQVAFITDPREGSSQYCTDVAKALSAPIFHVNADDIEAVVHAC	480
B-p-ox:	244	ALPNYCTGCTVHIVVNQVAFITDPREGSSQYCTDVAKALSAPIFHVNADDIEAVVHAC	303
At-ox:	481	ELAAEWRTFHSDDVVDLVCYRRFGHNEIDEPSFTQPKMYKVIKSHPSLQIQEKLQS	540
B-p-ox:	304	ELAAEWRTFHSDDVVDLVCYRRFGHNEIDEPSFTQPKMYKVIKSHPSLQIQEKLQS	363
At-ox:	541	GOVTQEDIDKIQKVSILNEEYASKDYIPQKRDWLASHWTGFKSPEQISIRINTGVKP	600
B-p-ox:	364	GOVTQEDIDKIQKVSILNEEYASKDYIPQKRDWLASHWTGFKSPEQISIRINTGVKP	423
At-ox:	601	EILKRVGKAISTFPENFKPHRGVVKRYEQRAQMIESGEGIDWGLGEALAFATLVEGNHV	660
B-p-ox:	424	EILKRVGKAISTFPENFKPHRGVVKRYEQRAQMIESGEGIDWGLGEALAFATLVEGNHV	483
At-ox:	661	RLSGQDVERGTFSHRHSLVLDQETGEFYCPDLHLIKNODPEMFTVSNSLSSEFVGLGFEL	720
B-p-ox:	484	RLSGQDVERGTFSHRHSLVLDQETGEFYCPDLHLIKNODPEMFTVSNSLSSEFVGLGFEL	543
At-ox:	721	GYSMENPNSLVIWEAQFGDFANGAQMFDQFISSEGAQWLRQTGLVVLPHGYDGGQPEH	780
B-p-ox:	544	GYSMENPNSLVIWEAQFGDFANGAQMFDQFISSEGAQWLRQTGLVVLPHGYDGGQPEH	603
At-ox:	781	SSGRLEFLQMSDDNPYVIPMDPTLRKQIQECNQVNVNVTTPANYFHVLRRIHRDFRK	840
B-p-ox:	604	SSGRLEFLQMSDDNPYVIPMDPTLRKQIQECNQVNVNVTTPANYFHVLRRIHRDFRK	663
At-ox:	841	PLIVMAPKNLLRHKKCVSNLSEFDDVKGHPGFDKQGTFRFKRLIKDQSGHSDLEEGIRRLV	900
B-p-ox:	664	PLIVMAPKNLLRHKKCVSNLSEFDDVKGHPGFDKQGTFRFKRLIKDQSGHSDLEEGIRRLV	723
At-ox:	901	LCSGKVVYELDEERKKS+ DVAICRVEQLCPFPYDLIQRELKRYNPAEIVWCQEEPMNM	960
B-p-ox:	724	LCSGKVVYELDEERKKS+ DVAICRVEQLCPFPYDLIQRELKRYNPAEIVWCQEEPMNM	783
At-ox:	961	GGYQYIALRLCTAMKALQGNFNDIKYVGRLPAAATATGFYQLHVKEQTDLVKKALQPD	1020
B-p-ox:	784	GGYQYIALRLCTAMKALQGNFNDIKYVGRLPAAATATGFYQLHVKEQTDLVKKALQPD	843

At-ox: *Arabidopsis thaliana* 2-oxoglutarate dehydrogenase E1 subunit; GI: 18389253

B-p-ox: Barley putative 2-oxoglutarate dehydrogenase; GI: 18235680, 14525312, 19520324, 18205270, 18206048, 9419194 and 18208234

Fig. 2. Amino acid alignment between the 2-oxoglutarate dehydrogenase E1 subunit (At-ox) and the barley homologue (B-p-ox). The barley 2-oxoglutarate dehydrogenase E1 subunit homologue is a composite constructed from overlapping sequences present in the database. Sequences obtained from four tryptic digests from the 110 kDa purified Pab240 cross-reactive polypeptide (P1–P4) were 100% identical with the under-scored sequence. Black box: Pab240 recognition site; white box: putative Pab122 recognition site.

found that this antibody recognises a five amino acid long epitope, RHSV(V/I), of human, mouse and chicken p53 [13]. In barley embryonic suspension cells, this antibody showed cross-reaction with several polypeptides ranging from 10 to 110 kDa. The cross-reaction with the small polypeptides, which were predominant in the cellular debris after centrifugation, was unspecific since cross-reaction was also observed by using only the secondary antibody GAM-HRP (Fig. 1). However, three polypeptides of 53, 73 and 110 kDa, respectively, present in the cytosolic fraction after centrifugation, specifically cross-react with the Pab240 antibody. Especially the 73 and 53 kDa polypeptides frequently appeared on blot

as doublets. The ratio between these three Pab240 cross-reactive polypeptides varied among different extracts we made. In order to find out whether these different polypeptides were related to each other and whether they represented plant p53-like proteins, a three-step purification protocol was developed as described in Section 2. The purification, as schematically depicted in Fig. 1, finally resulted in a purified 110 kDa polypeptide from the cytosolic extract which could be converted to the 73 and 53 kDa form by means of mild trypsin digestion. Both 73 and 53 kDa polypeptides were subjected to sequence analysis. First by peptide mapping it became clear that the doublets represent one and the same protein. Se-

quence analysis resulted in the identification of four peptides (P1–P4 in Fig. 2) which were all homologues to the *Arabidopsis* 2-oxoglutarate dehydrogenase. By searching for the barley homologue in the NCBI database we were able to retrieve seven expressed sequence tags which almost fully covered the entire protein (Fig. 2). Amino acid positions 498–502 of the barley composite exposes the sequence RHSV, indeed an epitope for Pab240 [13,14]. Moreover, positions 680–684 expose a putative epitope for another p53 monoclonal antibody, Pab122.

Independently of the protein purification as described above, another approach was followed to identify the Pab240 cross-reactive protein in barley. An expression library was constructed from the total mRNA pool isolated from a mixture of heat-shocked and control barley suspension cells. First we have checked whether cross-reactivity of Pab240 occurs in *Escherichia coli* cells, the host cells of the λ ZAP phages. No cross-reaction could be observed. After screening of the transfected library, several Pab240 cross-reactive clones were found and subsequently isolated. One strong cross-reactive clone was selected for sequence analysis. Again this sequence showed a strong similarity with the *Arabidopsis* 2-oxoglutarate dehydrogenase (Fig. 3). These data confirm the identity of the Pab240 cross-reactive protein in barley as obtained by protein purification.

Next we wanted to find out whether the 53, 73, both often appearing as a doublet, and 110 kDa polypeptides were related to each other or different proteins carrying an epitope for Pab240. It was shown that mammalian p53s exposing the pab240 epitope are able to associate with heat-shock protein hsp70 [12]. If we heat-shocked our barley cell suspensions (10 min 42°C) at several time points prior to protein extraction we could clearly demonstrate that both the 53 and 73 kDa cross-reactive bands disappear in favour of the 110 kDa band (Fig. 4). Moreover, if the heat-shocked sample containing the 110 kDa protein (or the 110 kDa protein isolated by preparative PAGE during the purification protocol) was treated with a low concentration of trypsin, the intensity of the 110 kDa band diminished and the 73 and 53 kDa bands appeared again on Western blot. The concentration of trypsin used in

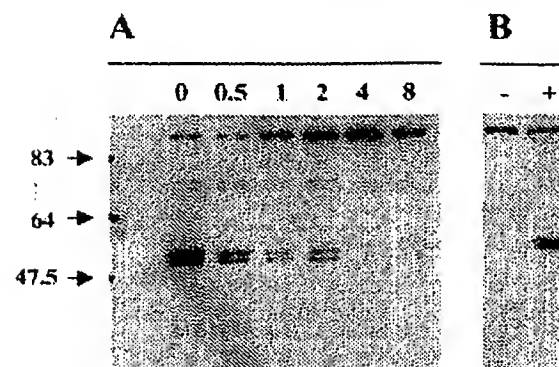


Fig. 4. A: Behaviour of the Pab240 cross-reactive polypeptides in cytosolic extracts of barley embryonic suspension cells after heat shock (10 min, 42°C). Cytosolic extracts were made prior to heat shock (0) and after 0.5, 1, 2, 4 and 8 h recovery at 28°C. B: Trypsin treatment of a cytosolic extract obtained from heat-shocked cells after 4 h recovery; (–) before trypsin treatment, (+) after 50 min incubation with 20 μ g/ml trypsin at 23°C. Both Western blots were probed with the Pab240 antibody.

these experiments was extremely critical since a small increase resulted in complete disappearance from the blot. These data strongly indicate that the 53 and 73 kDa polypeptides were degradation products of the 110 kDa polypeptide due to proteolytic activity during isolation. We suggest that binding of heat-shock proteins to the 110 kDa polypeptide in reaction to heat shock (Fig. 4A) may prevent this degradation. The fact that tryptic digests of the 53/73 kDa polypeptides, obtained during sequence analysis, display a high degree of homology with the 105 kDa 2-oxoglutarate dehydrogenase strongly supports this hypothesis.

4. Discussion

In this study we have demonstrated that the cross-reactivity with the p53-specific Pab240 antibody in barley was not caused by a putative plant p53 homologue but by 2-oxoglutarate dehydrogenase, a 105 kDa subunit from a multi-enzyme assembly that occupies a central role in cellular metabolism within the tricarboxylic acid cycle. The presence of this protein combined with its biochemical features during experimental conditions causes a big obstacle for identifying p53-like proteins in plants by using Western blot techniques only. It mimics the features of the mammal p53 in several ways:

First, there is a clear recognition of the plant 2-oxoglutarate dehydrogenase by one of the best studied and frequently utilised antibodies in mammalian p53 research activities, the monoclonal Pab240. Obviously, this antibody may not be specific enough, since only a small motif of five amino acid residues, RHSV(V/I), also present at positions 498–502 of the barley 2-oxoglutarate dehydrogenase composite, allows recognition by the antibody [13,14]. It was already demonstrated that proteins containing this motif, like TFIIIA from *Xenopus laevis*, cross-react with the Pab240 [13]. Referring to Stephen et al. [14], a second interesting motif may be present on the barley 2-oxoglutarate dehydrogenase composite, KSSL, located at positions 681–685, which mimics an epitope for the p53 monoclonal Pab122 [14]. Interestingly, in pea root tips a 94 kDa protein was recognised by both Pab240 and Pab122 antibodies [5]. However, due to limited information on the Pab122 epitope, the lack of sequence information of the pea oxoglutarate dehydrogenase homologue and the fact that dif-

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PRC : 509  tcttgggttgaattgggctactccatggagaacccaattcgctagctactctgggaagc
At-ox: 2260  tctcgggttgcgaactgggttatcgatgggaacccaattctctgggtgatatgggaagc
715  L G F E L G Y S M E N P N S L V I W E A

PRC : 569  tcagtttgggtgactgccccaatggtagcacaagtgcgttcgaccatctactgagtagay
At-ox: 2320  tcagtttgggtgactgccccaatggtagcacaagtgcgttcgaccatctactgagtagay
735  Q F G D F A N G A Q V M F D Q P I S S

PRC : 629  gagatgcaaaatggctgcg-catactggccttgcgttcactgcctcatggttatgatg
At-ox: 2379  ggaagtcgaaatggctgcg-catactggccttgcgttcactgcctcatggttatgatg
754  G E A K W L R Q T G L V V L L P H G Y D

PRC : 688  gtcaaggtcctgaacactctagctccttttttaggatcgcttgcgttgagatgagtgatgac
At-ox: 2439  gtcaaggtcctgaacactctagctccttttttaggatcgcttgcgttgagatgagtgatgac
774  C Q G P E H S S G R L E R F L Q M S D D

PRC : 748  aatacttactgactactacatgatggaccca 777
At-ox: 2498  aatacttactgactactacatgatggaccca 2527
794  N P Y V I P K M D P

PRC : Pab240 Reactive Clone from barley expression library
At-ox: Arabidopsis thaliana 2-oxoglutarate dehydrogenase E1 subunit; GI: 18389253

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Fig. 3. Nucleotide sequence alignment between a clone isolated from the barley expression library, cross-reacting with the Pab240 antibody (PRC), and the 2-oxoglutarate dehydrogenase E1 subunit from *Arabidopsis thaliana* (At-ox). 81% identity was obtained.

ferent experimental procedures were used as compared to our study, it is not possible to predict whether cross-reactivity in pea is also caused by oxoglutarate dehydrogenase.

Second, we observed a dramatic increase in intensity of the Pab240 cross-reactive bands during the early stage of germination. In this period the machinery of DNA repair, to recover DNA integrity induced during seed maturation and storage [7,8], is fully operable. In mammalian cells p53 induces G1 arrest to allow DNA repair, so indeed one expects to find an increase of the putative plant p53 during early germination. On the other hand, during early germination also the plant cellular metabolism is fully switched on, e.g. enzymatic activity in the tricarboxylic acid cycle. Consequently, it remains unclear whether the observed increase of the Pab240 cross-reactive bands during the early stage of germination is a result of an increase of p53-related proteins involved in DNA repair or just an increase of the metabolic enzyme oxoglutarate dehydrogenase.

Third, the molecular weight of the Pab240 cross-reactive proteins in plant extracts under denaturing conditions is similar to that of mammalian p53. However, next to a 53 kDa band, a 73 and 110 kDa band were also recognised in barley extracts by the Pab240 antibody. Interestingly, the ratio of the intensity of those 53, 73 and 110 kDa bands varied within the several extracts we made. Cross-reactivity in the region of 70 and 100 kDa by the Pab240 antibody was already reported to occur in maize [3] and pea [5,6]. In this report we showed that in our experimental system, the cytosolic extract of barley suspension cells, the 53, 73 and 110 kDa bands are related to each other. Artificial proteolytic cleavage of the purified 110 kDa band by controlled trypsin digestion revealed that the 110 kDa band could be easily converted to the 73 and 53 kDa form. Moreover, with heat-shock treatment of the barley suspension cells we showed that the intensity of the 53/73 kDa bands isolated during extraction decreased dramatically in favour of the 110 kDa band. Furthermore, it was shown by Gannon et al. [12] that proteins exposing the Pab240 epitope RHSV(V/I) were able to bind heat-shock protein hsp70. These chaperones are highly conserved proteins among the animal and plant kingdom. Assuming that 2-oxoglutarate dehydrogenase exposes its RHSVI motif, the hsp70, probably present in a chaperone complex, may associate and consequently stabilise the protein, thereby preventing proteolytic cleavage during isolation, especially after heat shock. It may be interesting to note that during purification of the 110 kDa polypeptide the heat-shock protein hsp82, a member of the hsp90 family, was co-purified (data not shown). It is known that chaperone complexes may contain both hsp90 and hsp70 proteins and that these complexes are evolutionarily conserved between the animal and plant kingdom [15]. Taken together, there are strong indications that the 53, 73 and 110 kDa polypeptides represent one and the same protein, the 105 kDa 2-oxoglutarate dehydrogenase.

The fact that the Pab240 cross-reactive protein(s), obtained by protein purification as well as by screening of an expression library, was identified as 2-oxoglutarate dehydrogenase, does not exclude the possibility that more Pab240 cross-reacting proteins or even p53-related proteins exist in plant cells. For example, 2-oxoglutarate dehydrogenase is a metabolic protein present in a complex in the mitochondria, but in pea cross-

reactivity with the Pab240 was also observed in nuclei by means of immuno-localisation studies [5]. However, extreme caution must be taken by interpretation of data only obtained by immunological experiments. In our opinion, the putative plant p53, if it exists, will be a functional homologue rather than a structural one. Searching for sequence homology in plant nucleotide databases failed thus far and moreover, even among animals the p53 protein is not highly conserved. Only recently the p53 homologues of *Drosophila melanogaster* [16–18] and *Caenorhabditis elegans* [19] were identified. From these studies it became clear that only a set of five domains of the p53 were conserved. The p53 homologue of *C. elegans* could not be retrieved from public databases using standard searches and only with additional algorithms the conserved domains and therefore the p53 homologue could be identified [19]. Still, even by using these conserved domains and the additional algorithms for searching in plant databases, a plant p53 homologue could not be found. Focussing on p53's interacting partners, like the highly conserved proteins involved in cell-cycle regulation or inhibitory proteins might be a fruitful strategy for identifying the plant p53 homologue.

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